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AC012107 Homo sapi
AL139089 Human DNA
AL196266 Human DNA
AC010801 Homo sapi
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119458 CCAGGTACTCAGCCATGTGCTGGGCCATGGGAACCCCAAATATTAATAAGACATTGTCAGG
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Quality: Phrap Quality >=40 99.9% of Sequence;

Estimated Total Number of Errors is 0.3.

NOTE: Transposon sequencing failed to verify the number of repeat copies 67315-69359. Unsure number of repeat copies 67315-69359. Unsure number of repeat copies 67315-69359. Unsure number of repeat copies 67315-69359.

NOTE: Shatter libraries failed to resolve dinucleotide repeat region 171590-171722. Unsure number of repeat copies

171590-171722. Forced join 171695.

Location/Qualifiers
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Submitted (16-AUG-2002) DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Aug 16, 2002 this sequence version replaced gi:15022008.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
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Submitted (07-0CT-1999) Production Sequencing Facility, DOE (
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9459)
3 (bases 1 to 187064)
DOE Joint Genome Institute and Stanford Human Genome Center.
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1 (bases 1 to 187064)

DOE Joint Genome Institute

Direct Submission
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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DOE Joint Genome Insti
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                                                                                                          AGCCGGAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTG
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67315. .69359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="NOTE: Shatter libraries failed to resolve dinucleotide repeat region 171590-171722. Unsure number of repeat copies 171590-171722. Forced join 171695."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .187064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 398; DB 5; 1
Pred. No. 5.2e-128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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Creek, CA 94598, USA
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                                                                                                                   119757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              119577
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Insert size: 236000; agarose-fp
Insert size: 204523; sum-of-contigs
Quality coverage: 6.54 in Q20 bases; agarose-fp
Quality coverage: 7.57 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: plasmid; 16% Chemistry: Dye-primer ET, 84% of reads Chemistry: Dye-terminator Big Dye; 16% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 199676 bases at least Q40 Consensus quality: 200928 bases at least Q30 Consensus quality: 201749 bases at least Q20 Consensus quality: 201749 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (30-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Aug 17, 2000 this sequence version replaced gi:9280808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC019238 204340 bp DNA linear HTG 17-AUG-2000 Homo Bapiens chromosome 19 clone RP11-700B5, WORKING DRAFT SEQUENCE, 12 unordered pieces.
AC019238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Washington University Genome Sequencing Center Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 204340)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 204340)
Waterston, R.H.
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HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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                                                                                                                                                                                  2752: contig of 2752 bp in length 2852: gap of unknown length 5901: contig of 3049 bp in length 6001: gap of unknown length length 606 bp in length 606 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Center -----
                                                    5: gap of unknown length
8: contig of 7953 bp in length
9: gap of unknown length
9: contig of 9281 bp in length
9: gap of unknown length
9: gap of unknown length
9: gap of inknown length
                      gap of contig
unknown length
of 11122 bp in
unknown length
                 length
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Best Local Similarity
Matches 231; Conserv
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168 AACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGGCATGGTGGCACACACCTGTAGTC 227
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65276
65376
95162
95262
122539
122539
152779
                                       Conservative
                                                                                                                                                                                                 vector side:right"
155779. .155878
/estimated length=unknown
155879. .204340
                                                                                                                                        /note="assembly_name:Contig27
clone_end:SP6
vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52181. .52280
/estimated_length=unknown
52281. .65275
                                                                                                                                                                                                                                                                                       Clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                            95262. .122538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /estimated_length=unknown
41059. .52180
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
                                                                                                                                                                                                                                                                                                                                      22639. .155778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5276. .65375
                                                                                                                                                                                                                                                                                                             note="assembly_name:Contig26
                                                                                                                                                                                                                                                                                                                                                       estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                                               note="assembly_name:Contig25'
22539. .122638
                                                                                                                                                                                                                                                                                                                                                                                                                                             estimated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_name:Contig22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0500. .40958
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1853. .5901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="assembly_name:Contig24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="assembly_name:Contig21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="assembly_name:Contig19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="assembly_name:Contig18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="assembly_name:Contig17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   estimated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="assembly_name:Contig20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       estimated
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65375: gap of unknown length
95161: contig of 29786 bp in length
95261: gap of unknown length
122538: contig of 27277 bp in length
122638: gap of unknown length
155778: contig of 33140 bp in length
155878: gap of unknown length
155878: gap of unknown length
155878: gap of unknown length
204340: contig of 48462 bp in length.
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                                                         57.8%;
99.1%;
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_.95161
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                                     1; Mismatches
                                                         Score 231; DB 12;
Pred. No. 8.9e-69;
                                       1;
                                                                             Length 204340;
                                       Indels
                                     0;
                                     Gaps
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JOURNAL

AUTHORS TITLE

JOURNAL

COMMENT

2753 2853 5902 6002 12966 13066 21019

30500

REFERENCE AUTHORS TITLE

KEYWORDS SOURCE

ORGANISM

Homo sapiens

lominidae; Homo

ACCESSION VERSION

RESULT 2 AC019238

DEFINITION Snoo 뭉 8

119818 361

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JOURNAL REFERENCE
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AUTHORS
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KEYWORDS
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AC146499/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Direct Submission
Genome Sciences, Lawrence Submitted (21-AUG-2003) Genome Sciences, Lawrence Submitted (21-AUG-2003) Genome Sciences, CA 94720, U
Chemistry: Dye-terminator Big Dye
Assembly program: Phrap version 0.990329.

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 2 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence Produced by Berkeley Web site: http://pga.lbl.gov Center Code: PGABERK Center Project Name: W033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peng,Z., Malinov,I. and Rubin,E.M.
Direct Submission
Submitted (26-NOV-2003) Genome Sciences, Lawrence Berkeley National
Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 184822)
Cheng, J.-F., Hamilton, M., Peng, Y., Peng, Z., Malinov, I. and Rubin, E.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC146499.1 GI:34013545
HTG; HTGS_PHASE2; HTGS_DRAFT.
Aotus nancymaae (Ma's night monkey)
                                                                                                                                                                                                                                                                                                                                                                                       This sequence has been compared to sequences of other species using Vista (http://www-gsd.lbl.gov/VISTA). The results can b
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheng, J.-F., Hamilton, M., Peng, Y., Peng, Z., Malinov, I. and Rubin, E.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aotus nancymaae
                                                                                                                           Sequencing vector: Plasmid, pUC18
                                                                                                                                                      Summary Statistics:
                                                                                                                                                                                            Funding agent: Programs for Genomic Applications (NHLBI)
                                                                                                                                                                                                                                                                                                      The order-orientation of the draft sequence was accomplished
                                                                                                                                                                                                                                                                                                                                                http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=APOA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cheng, J.-F., Hamilton, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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1 (bases 1 to 184822)
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Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aotus nancymaae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone Name:
                                                                                                                                                                                                                                     (http://baboon.math.berkeley.edu/mavid), (http://lagan.stanford.edu/) and paired
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1 Rubin,E.M.
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USA
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SEQUENCE, 2
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                      TITLE
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Pongo pys
                                                                                                                         Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B., Coleman, H., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B., Idol, J.R., Karlins, E., Kwong, P., Laric, P., Larson, S., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, M., Mullikin, J.C., Paguirigan, C., Pearson, R., Portnoy, M.B., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Young, A. and Crons, P.
    Green, E.D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC146898.3 GI:38638702
HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                       NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                   Hominidae; Pongo.
1 (bases 1 to 232406)
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pongo pygmaeus
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pongo pygmaeus (orangutan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC146898
                                                                 Unpublished
                                                                                                           Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the gaps between them are based on estimates provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available the accession number will be preserved.

1 32135: contig of 32135 bp in length 32136 32235: gap of unknown length 32236 184822: contig of 152587 bp in length 10cation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTGAACCCAGGAGGCGGAGGTTGCACTCCAGCCTGGGTAACAAGAGTGAAACTCTGTCT 133549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGGATCAC--GAGGTCAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGAGACCATCCTGGTCAACATGGTGAAAACCCCGTCTCTACTAAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAAAACAACAACAAAAAACAAAAAACCATAAGACAT
                                          (bases 1 to 232406)
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/mol_type="genomic DNA"
/db_xref="taxon:37293"
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                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232406 bp
CH253-50L14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 161.2; DB 1
Pred. No. 4.7e-44;
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WORKING
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DRAFT SEQUENCE, 4 ordered
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Masiello,C.,
Pearson,R.,

2:

Gaps

140

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260

133669

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FEATURES
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                                                                                                                                                                                                                                                              misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with
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3 (bases 1 to 232406)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the accession number will be preserved.

1 80408: contig of 80408 bp in length
80409 80508: gap of unknown length
101957: contig of 21449 bp in length
102057: gap of unknown length
102058 206149: contig of 104092 bp in length
206150 206249: gap of unknown length
206250 232406: contig of 26157 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps here the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 231482 bases at least Q40
Consensus quality: 231897 bases at least Q30
Consensus quality: 232064 bases at least Q20
Insert size: 245000; agarose-fp
Insert size: 232106; sum-of-contiss
Quality coverage: 21.15x in Q20 bases; sum-of-conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a Phrap-derived quality score.
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80509. .10195/
/note="assembly_fragment"
'no1958. .102057
                                                                                                                                                              vector_side:left"
                                                                                                                                                                                                        clone_end:T7
                                                                                  /estimated_length=unknown
80509. .101957
                                                                                                                                                                                                                                                                                                                          /organism="Pongo pygmaeus"
/mol_type="genomic DNA"
/db_xref="taxon:9600"
/clone="CH253-50L14"
                                                                                                                                                                                                                              note="assembly_fragment/
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                                                                                                                                                                                                                                                                                             clone_lib="CH253"
                                                                                                                                           80508
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                                                                                             Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barra, N., Beckerly, R., Benn, J., Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Colling, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Donelan, L., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Geralgery, K., Grant, G., Hagos, B., Heaford, A., Herena, L., Horton, L., Howland, J.C., Jacotot, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Molla, M., Morris, M., Morrow, J., Mychaleckyj, J., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Vassilley, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W.J., Zhao, J. and Zody, M.
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Submitted (19-AUG-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 97676)
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone RP11-952N18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Homo sapiens chromosome 17, clone RP11-952N18, complete sequence.
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clone_end:SP6
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Pred. No. 8.6e-44;
1; Mismatches 60
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region	Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu	Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'O'Donell, P., O'O'Donell, P., O'O'Donell, P., O'O'Donell, P., O'O'Donell, P., O'O'Donell, P., O'Donell, P., O'O'Donell, P., O'Donell, P., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Talor, R., Rogov, P., Rothman, D., Yessilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M. TITLE Direct Submission Submitted (17-JUN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA On Jun 17, 2000 this sequence version replaced gi:7139014. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html Only 97676 base pairs from the middle of this clone are being submitted. The remainder overlaps either accession AC015842 (WICGR project L449) or accession AC005304 (WICGR project L356). 850 base pairs into the overlap with L449 [not submitted] is a VNTR that has been expanded by approximately 2.1 kilobases relative to project L449. Genome Center	AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Looke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
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            Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Feb 5, 2001 this sequence version replaced gi:12581050. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                       AL445686 107868 bp DNA linear PRI 18-MAY-2005 Human DNA sequence from clone RPII-496D1 on chromosome 1 Contains the gene for a novel protein (FLJ45258), a ribosomal protein L26 (RPL26) pseudogene, the 5' end of the SRRWI gene for serine/arginine repetitive matrix 1 and a CpG island, complete
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                                                                                                                                                                          Direct Submission
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Mammalia; Eutheria;
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Pred. No. 9.3e-44;
1; Mismatches 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RP11-496D1 is from the library RPCI-11.2 constructed of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Wellcome Trust
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              was generated from part of bacterial clone contigs of human
62744. .62749
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                                                                                                                                                                                                                                                     locus_tag="RP11-496D1.
standard_name="OTTHUMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      locus_tag="RP11-496D1.2-001"
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                                                                                                                                                                                                                                                                                                                                                                              ocus_tag="RP11-496D1.1-002"
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                                                                                                                                                                                                                                                       _name="OTTHUMP00000003372"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="serine\/arginine repetitive matrix 1"
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105870. .106064,106349. .105468,AL445648.18:2823. .2697
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105870. .105950)
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102295. .102465,103407. .103468)
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105870. .105950)
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105870. .105978)
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join(96709. .96783,99420. .99509,100103.
102295. .102391,103470. .103522,104845.
105870. .105978)
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                        JOURNAL REFERENCE
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AUTHORS
TITLE
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ORGANISM
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DEFINITION
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AC016542
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Best Local
      AUTHORS
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    Unpublished
2 (bases 1 to 171480)
Smith, D.R.
                                                                                                                                                                                                                                                            Homo sapiens chromosome 10
AC016542
AC016542.11 GI:19744959
HTG.
                                                                                                                                                                                                                  Homo sapiens
                                                                  Sequence Data
                                                                                          Genome Therapeutics Corporation
                                                                                                            Smith, D.R.
                                                                                                                                                      Hominidae; Homo.
                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                        Homo sapiens (human)
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                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                             clone RP11-354E23, complete sequence.
                                                                                          Sequencing
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Center: Human Genome

linear

PRI 09-APR-2002

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22531 CTTGACCCCAGAGGTTGCAGTGAGCTGAGATCGCACCATTGGGCGACAGAGCAAGTCTCC
AAAAAAAAACAAAACAAAACAAATATATTAGGAATTAAAAGCTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                             TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATTACAAAAATAGC 200
                                                           CAAAAACAACAAAAAAAAAAAAAAAAACCATAAGACATTGTCCATCTGCGG 371
                                                                                                                                                                                                                                          CGGGCATGGTGGCAGGCGCCTGTAATCTCAGCTACTCGGGAGGCTGAGGTGGGAGAATTG 22532
                                                                                                                                                                                                                                                                            TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                                                                                                                                                           ATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCAGGTGAGGTCAGGTCAGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
                                                                                                                                                                            TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Join(96735. .96783,99420. .99509,100103. .100225, 102295. .102465,103407. .103522,104845. .105048, 105870. .106064,106364. .1054648, L1445648.18:8287. 8367, AL445648.18:8287. 8367, AL445648.18:8878. 8964, AL445648.18:10228. .10372, AL445648.18:10751. .10792, AL445648.18:1433. .14493, AL445648.18:16691. .17155, AL445648.18:17688. .17883, AL445648.18:16691. .17155, AL445648.18:19780. .17883, AL445648.18:18954. .19163, AL445648.18:19780. .20830)
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/note="match: ESTs: Em:CD656593.1
match: cDNAs: Em:AK032599.1"
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/product="serine\/arginine repetitive matrix 1"
/note="match: ESTs: Em:BG700853.1"
/loin 96729. .96783,99420. .99509,100103. .102465
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join(96729. .96783,99420. .99509,
103407. .103522)
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On Mar 27, 2002 this sequence version replaced gi:16930889.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (28-MAR-2002) Genome Therapeutics Corporation, Street, Waltham, MA 02453, USA 6 (bases 1 to 171480)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (15-NOV-2001) Genome Street, Waltham, MA 02453, USA (bases 1 to 171480)
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                                                                                                                                                                                                                                                                                                                       Similarity
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CAAAAACAACAACAAAAAAAAAAAAAACCATAAGACATTGTCCATCTGCGGTTCCCAGAC 380
                                                                                                                                                                                                                                                           CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTTGGGCGGATCACCTGAGGTCAAGAGATCG 143
                                                GAACCCAGGAGGCGGATTGGTTCTGCATTCTAGCCTAGGTGACAGAGTGAGACTCCGTCT
                                                                                                                                            GCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGA 263
                                                                                                                                                                            AGACCAGCCTGGGCAACATGGTGAAACCCCCGTCTCTACTAAAAATATAAAAATTAGCTGG
                                                                                                                                                                                                                                         CATGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACCTGAGGTCAGGAGTTCG 116855
                                                                             GATCGCAGAGTGAGCCGAAATCACAGATCACAG---AGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                             GCATGGTGGCATGTGCCTGTAATCCCAGCTACCCGGGAGGCTGAGGCAGGAGAATAGCTT 116975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.genomecorp.com/
Contact: gtc-seqcenter@genomecorp.com
Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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/clone_lib="RPCI-11"
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Pred. No. 1.4e-43;
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Li Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requestes: clonerequest@sanger.ac.uk

On Nov 2, 1997 this sequence version replaced gi:2462400.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: PMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/Celegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22

Mapping Group. Purther information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             one subclone; and the assembly was confirmed by restriction digest except on the rare occasion of the clone being a YAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/HGP/Chr22
RP3-408N23 is from the library RPCI-3 constructed by the group
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.sanger.ac.uk
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Mammalia; Eutheria;
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complement(AL049764.4:12691. .22186))
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/locus_tag="RP3-362J20.1-001"

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join(complement (34109. .34162), complement (13937. .13997), complement (AL049764. 4:12691. .20196), complement (AL049764. 4:22070. .22186), complement (AL049764. 4:22070. .22186), complement (AL049764. 4:13989. .17080), complement (AL049764. 4:13989. .17080), complement (AL049764. 4:13989. .17080), complement (AL049764. 4:13989. .14042))
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71345. .71758))

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FQDVAQNPANMSKYQSNPKVMNLISKLSAKFGGQA"
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                                                                                                                                                                                                                                                                              RESULT 9
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Query Match
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                                                                                                                                                                                                                                                                     TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAAATAGC
                                                                                                                                                                                                                                                                                                                       CAAAAAAAAAAAAAAAAA 11547
                                     САААААСААСААСААААА 339
                                                                               CGTGAATCCAGGCCGAGATTGTGCCACTGCACTCCAACCTGGGTAAGAGAGACTCTGTCT 11528
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75.7%;
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Pred. No. 1.5e-43;
1; Mismatches 62;
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Homo sapiens chromosome 11 clone RP11-804A23 map 11, WORKING DRAFT SEQUENCE, 10 unordered pieces.

AC090344
AC090344.3 GI:14626339

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COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is architrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 7, 2001 this sequence version replaced gi:13357354. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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1 (bases 1 to 195616)

Birren,B., Linton,L., Nusbaum,C. and Lander,B.
Homo sapiens chromosome 11, clone RP11-804A23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: 804 A 23

Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 191318 bases at least Q30

Consensus quality: 193221 bases at least Q30

Consensus quality: 194120 bases at least Q20

Insert size: 194716; sum-of-contigs

Quality coverage: 9.4 in Q20 bases; sum-of-contigs
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                         be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
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9269: contig of 9269 bp in length
9369: gap of 100 bp
10358: contig of 989 bp in length
10458: gap of 100 bp
13550: contig of 3092 bp in length
13650: gap of 100 bp
26222: contig of 12572 bp in length
26322: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9370. .10358
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                          note="assembly_fragment
                                                                                                  146366. .18056
                                                                                                                            'note="assembly_fragment"
|46266. .146365
                                                                                                                                                                                    note="assembly_fragment"
|20503. .120602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                estimated_length=100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="RP11-804A23"
clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                               note="assembly_fragment"
                                                                                                              estimated
                                                                                                                                                                     estimated_length=100
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                                                                                                              _length=100
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gap of 100 bp
contig of 25663 bp i
gap of 100 bp
contig of 34199 bp i
                                                                                                                                                                                                                                                                                                                                          length=100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of 60100 bp i
gap of 100 bp
contig of 14476 bp i
gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                  length=100
                                                                                                                                                                                                                                                                                  length=100
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141 TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAAATACAAAAAAATAGC 200

81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140

Similarity

39.7%;

Score 158.8; DB 1 Pred. No. 3.5e-43; Mismatches

DB 12; Length 195616;

Indels

7; Gaps

Conservative

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JOURNAL
REFERENCE
AUTHORS
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
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AC090345/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C., H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, M., Travis, N., Trajamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trajamas, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91427
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                                                                                                                                                                                                                                                                                                                                                Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 11, 2001 this sequence version replaced gi:13357355. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, College, College, College, College, College, 
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-804B24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGCATGGTGGCACACCTGTAGTCCCCAGCTACTCAGGA-----GCCGGAGATTGC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 197156)
                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L12623
------ Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                           Center clone name: 804_B_24
                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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sapiens chromosome 11 clone RP11-804B24 map 11, WORKING DRAFT
ENCE, 10 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150257
182158
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21901. .61396
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11370. .11469
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                                          /note="assembly_fragment"
124356. .124455
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/clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"/mol_type="genomic DNA"
                                                                                                                                               estimated_length=100/
                                                                                                                                                                                                           'note="assembly_fragment"
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11469: gap of 100 bp
14984: contig of 3515 bp in length
15084: gap of 100 bp
21800: contig of 6716 bp in length
21900: gap of 100 bp
61396: contig of 39496 bp in length
61496: gap of 100 bp
83042: contig of 21546 bp in length
83142: gap of 100 bp
97779: contig of 14637 bp in length
97879: gap of 100 bp
124455: gap of 100 bp
124455: gap of 100 bp
150156: contig of 25701 bp in length
150256: gap of 100 bp
182157: contig of 31901 bp in length
182257: gap of 100 bp
182157: contig of 31901 bp in length
182257: gap of 100 bp
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Best Local Simi
Matches 216;
                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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                                                                                                                                                                                                              Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. a Homo sapiens genomic DNA Published Only in Database (1999)

2 (bases 1 to 197856)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. a Direct Submission
                                                                                                               and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel.81-45-503-9111, Fax:81-45-503-9170)
                                                                                               Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens genomic DNA,
                                                                                                                                                                                          Submitted (25-NOV-1999) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Location/Qualifiers
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vector_side:right"
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182258. .197156
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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182158. .182257
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|50157. .150256
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74.0%;
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Pred. No. 3.5
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NNA, chromosome 11 clone:RP11-804A23, complete
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                                                                                             replaced gi:23821512
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and Sakaki, Y.
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RESULT 12
AC087662/c
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                                                                        JOURNAL
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                                                                                                      Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barra, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chopp, I.Y., Colangelo, M., Collins, S., Colymore, A., Cooke, P., Dakrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPhaeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Shauer, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Sutrauss, N., Sutrauss, N., Triaylis, N., Triglio, J., Vassillev, H., Viel, R., Vo, A., Zembek, L., Zimmer, A. and Zody, M.
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Submitted (15-JAN-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens Chromosome 8, clone RP5-1155K23 Unpublished
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Birren, B., Linton, L.,
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Homo sapiens chromosome 8 clone
                                                                                               Direct Submission
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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* NOTE: This record contains 84 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
                                                                                                                                                                                                                                                                                                                                   unclassified sequences.
1 (bases 1 to 96593)
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JP 2005510225-A/16.
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                                                                                            /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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2: contig of 671 bp in length
2: gap of 100 bp
4: contig of 742 bp in length
6: gap of 100 bp
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7: contig of 717 bp in length
7: contig of 717 bp in length
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8: contig of 717 bp in length
9: contig of 713 bp in length
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                        Score 158.4; DB 2;
Pred. No. 3.4e-43;
1; Mismatches 57;
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Sequence 1268 from Patent WO03008583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morris,D.W. and Engelhard,E.K.
Novel compositions and methods for cance Patent: WO 03008583-A 1268 30-UAN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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GTGAGACTTCATCTCAAAAAAAAACAAAAAACAAAAAACCAAGATG 18504
                      GTGAGACKCCGTCTCAAAAAACAACAACAAAAAACAAAAAAAAACCATAAG 354
                                                                                     TGAGATCGCAG------AGTGAGCCGAAATCACAGATCACAGAGTGAGCAGA 306
                                                                                                                                 TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
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/db_xref="taxon:9606"
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Pred. No. 3.4e-43;
1; Mismatches 57
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RESULT 15 AC010677/c

LOCUS DEFINITION

AC010677 112659 bp Homo sapiens chromosome 7 clone

CTD-2304L4, complete sequence.

linear PRI 03-JAN-2002

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Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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4 (bases 1 to 112659)
Waterston, R.
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Submitted (30-NOV-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MO 63108, USA
3 (bases 1 to 112659)
Waterston, R.H.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Submitted (17-SEP-1999) Genome
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1 (bases 1 to 112659)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: H_MS2304L04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: submissions@watson.wustl
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Waterston, R.H.
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AC010677.4 GI:11465112
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/db_xref="taxon:9606"
/chromosome="7"
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Submitted (18-JUL-2001) DOE Jo.
Drive, Walnut Creek, CA 94598,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (22-MAR-2000) Production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 945: 3 (bases 1 to 15344)
DOE Joint Genome Institute and Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu Quality: Phrap Quality >=40 99.8% of Sequence; Estimated Total Number of Errors is 0.2.
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DOE Joint Genome Institute and Stanford Human Genome Center
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DOE Joint Genome Institute.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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WI-6759 G05738
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                                                                                     TCGAGACCATCCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
 TGGGCATGGTGGCAGGGCCTGTAATCCCCAGCTACTCAGGAGGCGGAGGTTGCAGTGAGC
                     TGGGCATGGTGGCACACCTGTAGTCCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
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/clone="CTC-370J7"
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Submitted (03-MAY-2002) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
4 (bases 1 to 170154)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (29-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 29, 2003 this sequence version replaced gi:27819471.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (22-JAN-2003) Production Sequencing
Genome Institute, 2800 Mitchell Drive, Walnut
5 (Dases 1 to 170154)
DOE Joint Genome Institute, Stanford Human Gen
Alamos National Laboratory.
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DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                               Quality: Phrap Quality >=40 100%
Estimated Total Number of Errors
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                                                                                                                                                                                                                                                                                                                                  National Laboratory
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DOE Joint Genome Institute,
Alamos National Laboratory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC040168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACO40168 170154 bp
Homo sapiens chromosome 16 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC040168.8
                                                                                    Similarity
ACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGGGCAGATCAC--GAGGTCAAGAGA 134378
                    ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAAAAAAAAAAAAGACA 95559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAAAACAACAACAAAAAAACA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGAGATTG-----TGCCACTGCACTCCAGCCTGGGTGACAAGAGCAAAAACACTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 170154)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submission
                                                                                                                                                      organism="Homo sapiens"
/mol type="genomic DNA"
/db xref="taxon:9606"
/chromosome="16"
/clone="RP11-46107"
                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                .170154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:29366942
                                                                                  39.5%;
                                                                Score 157.8; DB 5;
Pred. No. 7.3e-43;
1; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone RP11-46107, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stanford Human Genome Center and
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                                                                                                                                                                                                                                                                                 ig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                 Sequence;
                                                                  Indels
                                                                                                   Length 170154;
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94598, USP
                                                                Gaps
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94598, USA
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94598, USA
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108
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REFERENCE
AUTHORS
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VERSION
KEYWORDS
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AC018605
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DE 3 (bases 1 to 186747)

S Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., LaRocque, K., Liamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Crant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., Pisani, C., Pollara, V., Raymond, C., Kiley, R., Rothman, D., Stojanovic, N., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., and Zody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Zimmer, A.
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1 (bases 1 to 186747)

Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 16, clone RP11-764C24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens chromosome 16 clone SEQUENCE, 15 unordered nianna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (14-DEC-1999) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC
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RP11-764C24
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COMMENT
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                                                                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: IA4986

Center clone name: 764 C 24

Center clone name: 764 C 24

Sequencing vector: M13; M77815; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 174578 bases at least Q40

Consensus quality: 179739 bases at least Q30

Consensus quality: 182173 bases at least Q20

Insert size: 188000; agarcse-fp

Insert size: 188347; sum-of-contigs

Quality coverage: 4.6 in Q20 bases; agarose-fp

Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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Center code: WIBR
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                                                       /organism="Homo sapiens"
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                                                                                                                                 110219: contig of 12406 bp in length
110319: gap of 100 bp
123656: contig of 13337 bp in length
123756: gap of 100 bp
138462: contig of 14706 bp in length
138562: gap of 100 bp
153566: contig of 15004 bp in length
153566: gap of 100 bp
153566: gap of 100 bp
180503: contig of 26837 bp in length
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180503: gap of 6144 bp in length
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7: contig of 33854 bp in length
7: gap of 100 bp
9: contig of 10372 bp in length
9: contig of 100 bp
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Query Match
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Best Local Similarity 75.8%; Pred. No. 7.6e-43;
Matches 207; Conservative 1; Mismatches 63; Indels 2; Gaps 1

Qy
81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGGTCAAGAGA 140

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AUTHORS
TITLE
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AUTHORS
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Submitted (23-DEC-2002) Production Sequencing Facility, DOE J
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598
5 (bases 1 to 198575)
DOE Joint Genome Institute, Stanford Human Genome Center and
                                                                                                                 www.jgi.doe.gov
Finishing Completed at
National Laboratory
                                                                                                                                                                           Drive, Walnut Creek, CA 94598, USA
On Mar 22, 2003 this sequence version replaced gi:27363205
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (06-FEB-2002) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA (bases 1 to 198575)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (06-MAY-1999) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, NM 87545, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chaster, J., Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Tatum, O., Campbell, C., Fawcett, J., Maltbie, M., Bussod, M., Sutherland, R., McMurry, K., Han, C. and Deaven, L.
                                                                                                                                                                                                                                          Direct Submission
Submitted (22-MAR-2003) DOE Joint Genome Institute,
                                  Quality: Phrap Quality >=40 100% of Sequence Estimated Total Number of Errors is 0. NOTE: BACTERIAL TRANSPOSON excised at 8530.
                                                                                                                                                                                                                                                                                     Alamos National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                         4 (bases 1 to 198575)
DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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AC007495
AC007495.9 GI:29150335
                                                                                              www-shgc.stanford.edu
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Alamos National Laboratory.
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Location/Qualifiers
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/db_xref="taxon:9606"
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Pred. No. 7.9e-43;
1; Mismatches 63
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REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION KEYWORDS COMMENT JOURNAL TITLE Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Oct 2, 2002 this sequence version replaced gi:23393869.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group Further information can be found at Human DNA sequence from clone RP13-444K19 on chromosome X Contains a mitochondrial ribosomal protein S18C (MRPS18C) pseudogene, the 3' end of the gene for a novel protein similar to PHD finger protein 2 PHF2 and a CpG island, complete sequence. Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX RP13-444K19 is from the library RPCI-13.2 co of Pieter de Jong. For further details see Homo sapiens Center code: SC Center: Wellcome Trust Sanger http://www.chori. VECTOR: pBACe3.6 Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Eukaryota; Metazoa; Mammalia; Eutheria; AL732374.14 GI:23476649 HTG; CpG island; MRPS18C; PHF2. Contact: vega@sanger.ac.uk Web site: Direct Submission Chapman, J. Hominidae; Homo. Homo sapiens (human) (bases 1 to 224187) //www.chori.org/bacpac/home.htm http://www.sanger.ac Genome Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Institute constructed λ the group

CDS

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FEATURES
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gene
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ORGANISM
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Direct Submission
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Forest Park Parkway, St. Louis, MO 63108, USA
On Oct 9, 2004 this sequence version replaced gi:51241995.
                                                                                                                                                Direct Submission
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Forest Park Parkway, St. Louis, MO 63108, USA
(bases 1 to 169908)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP. Pan troglodytes (chimpanzee)
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC150910 169908 bp
Pan troglodytes chromosome 7 clone
                                                                                                                        Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC150910.2 GI:54019620
                                                                                                                                                                                                                                                                         Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                               The sequence of Pan troglodytes clone
                                                                                                                                                                                                                                                                                                                                                                                              Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGAAAGAAAGAAAAGAAAAAA 191136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAGATCGCA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATGGCCAATATGGTGAAACCCCTGTCTGTACTAAAAATACAAAAATTAGCAGGGCATGGT 190998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCCAGCACTTTGGGAGGCCAAGGCAGGCAGATCACCTGAGGTCAGGAGTTCAAGACCAG 190938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGTCTAAAAAAGTATTTCAAGAAATAATGGCAGCCTGGCGCGCGGGCTCATGCCTGTAA 190878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACAAAAAACAAAAAAACCATAAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCACATGCCTGTAATCCCAGCTGCTCGGGAGGCCGAACACTGCAGTGAGCCGAGATCGCT 191058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCAT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCATGGT 210
                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 169908)
                                                                                                                                                                                                                                                                                                        (bases 1 to 169908)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OGKRPKKGLATAKORLGRILKIHRNGKLLL"

complement (join(128280. 129067,129799. 129908,

148509. 148604,170579. 170892,171481. 171614,

172743. 172828,173431. 173609,178401. 178504,

179266. 179568,181358. 181447,185535. 185626,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDDDDPALKSRPKKKKASDDAPWSPKARVTPTLPKQDRPVREGTRVASIETGLAAAAA
KLAQQELQKAQKKKYIKKKPLLKEVEQPRPQDSNLSLTVPAPTVAATPQLVTSSSPLP
PPEPKQEALSGSLADHEYTARPNAFGNAQANRSTTPMAPGVFLTQRRPSVGSQSNQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHEDEI PETVRTVQLI KOLARBI RLVEDI FQQNVGKTSNI FGLQRI FPAGSI PLTRPA
HSTSVSMSRLSLPSKNGSKKGLKFKELFKKAERKGKESSALGFAGQLSYNLMOTYSH
QALKTGSFQKAKFNI TGACLNINSDIODS PDLDLDGNESPLALMSNGSTRFKYKSLSKSR
RTKLAKKVDKARLMAEQVMEDEFDLDSDDELQ I DERLGKEKATLI I RPKFPRKLFRAK
FCSDPINTR PEGVET DI EED VT TDEDMYDEGVERSCHAGGGI LDLLKASRQVGGF
DYAALTEAPASFSTQBALGMLCMSANLOSSSSSFATSSLOAMWTGGDDRSSGSSSSSFL
DYAALTEAPASFSTQBALGMLCMSANLOSSSSFATSSLOAMWTGGDDRSGGSSGSSCB
OTVSNSPASORT FFGKRPI KRFAYWRTESEEEEENASLDEQDSLGACFKDAEYI VPSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.5%; Score 157.8; DB 5; 70.0%; Pred. No. 8.3e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA linear
CH251-484K21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 224187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Matches

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JOURNAL REFERENCE AUTHORS

REFERENCE AUTHORS

TITLE

ACCESSION VERSION

CEYWORDS

DEFINITION

REFERENCE AUTHORS TITLE

JOURNAL

JOURNAL

gap

gap

COMMENT

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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: plasmid; 100% Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.990319 Consensus quality: 164720 bases at least Q40 Consensus quality: 165787 bases at least Q30 Consensus quality: 166527 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: C_AB0484K21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site:http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Washington University
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: M13; 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as soon as it is available and the accession number will be preserved.
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21677
21777
21777
34794
34894
54354
54454
88285
88385
125438
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1482
7432
/estimated_length=unknown
54454. .88284
/note="assembly_name:Contig41"
                                                                         /note="assembly_name:Contig40"
54354. .54453
                                                                                                                                                            /note="assembly_name:Contig39"
34794. .34893
                                                                                                                                                                                                        /estimated_10
21777. .3479:
                                                                                                                                                                                                                                                                                  , carimated length=unknown
7532. .21676
                                                                                                                 34894. .54353
                                                                                                                                                                                                                                                                                                                                                                                                                       1482. .7431
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                                                                                                                                     estimated
                                                                                                                                                                                                                                                                note="assembly_name:Contig38"
                                                                                                                                                                                                                                                                                                                                                                                          note="assembly_name:Contig36
                                                                                                                                                                                                                                                                                                                                                                                                                                         estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="assembly_name:Contig31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="CH251-484K21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21676: contig of 14145 pp in renye...
21776: gap of unknown length
34793: contig of 13017 bp in length
34893: gap of unknown length
54353: contig of 19460 bp in length
54453: gap of unknown length
84284: contig of 3831 bp in length
88384: gap of unknown length
125437: contig of 37053 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125537: gap of unknown 169908: contig of 44371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               type="genomic
                                                                                                                                                                                                                                                  . .21776
                                                                                                                                                                                                                                                                                                                                                                             end:SP6
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                                                                                                                                                                                                                                                                                                                                                side:right"
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                                                                                                                                     length=unknown
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71 bp in
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RESULT 22
AC069513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
Mamminidae, Homo.

2E 1 (bases 1 to 174097)

1E 1 (bases 1 to 174097)

RS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Rs, Muzny, D.M., Adams, C., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Chen, R., Chen, R., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Davis, C., Davy-Carroll, L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gorrell, J.H., Guevara, W., Gunaratue, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., He, X., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Ummei, P., Howard, S., Huber, J., Hume, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC069513.28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC069513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAC Library)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACO69513 174097 bp DNA linear PRI 15-MAR-200.
Homo sapiens 3 BAC RP11-171N2 (Roswell Park Cancer Institute Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTGAACCCGGGAGGCAGAGGTTGCAATGAGCCGAGATCGTACCACTGCAATGCAGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCAGACTAT 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGAC 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGCATGGTGGCGGCACCTGTAGTCCCAGCTGCTTGGGAGACTGAGCCAGGAGAATTG 161530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KCCGTCTCAAAAAACAACAACAAAAAACAAAAAAACCATAAGACATTGTCCATCTGCGGTT 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCAGCGAAT 161400
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88385. 125437
/note="assembly name:Contig42"
125438 125537
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clone_end:T7
vector_side:left"
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125538. .169908
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Pred. No. 8.6e-43;
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Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovat, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L., C., Liu, J., L.Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mandiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Mirer, Z., Mitchell, T., Mohabbat, K., Moore, S., Morgan, M., Moorish, T., Morris, S., Moser, M., Neal, D., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G., Oragunye, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G., Oragunye, N., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Paychon, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Suton, A., Scherer, S., Soctt, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonake, T., Sparks, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Warf, M., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Walliams, G., Wang, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Direct Submission
Submitted (02-UUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Ravlor Plaza, Houston, TX 77030, USA
                         Worley,K.C.
Direct Submission
Submitted (15-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 28, 2002 this sequence version replaced gi:23343662.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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Direct Submission
Submitted (28-SEP-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 174097)
                                                                                                                                                                                                                                                                                                                          Submitted (28-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA bases 1 to 174097)
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Direct Submission
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gc-help@bcm.tmc.edu
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entire insert of this clone. Overlapping regions of clones are esquenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing. CLONE LENGTH: This sequence does not necessarily represent the clones are only ne remainder of

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. of a local database that includes entries from local mapping efforts. 7:541-550) searches dbSTS, GDB, and

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequences similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

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FRATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht
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                                                 complement (20877. .21305)
/rpt family="L2"
complement (21348. .21659)
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/rpt_family="Alusp"
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/rpt_family="AluSx"
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/rpt_family="MIR"
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'note="AC069513:G/AC112775:A/AC124944:A"
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              Direct Submission
Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joi
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598,
3 (bases 1 to 209844)
                                                                           2 (bases 1 to 209844)
DOE Joint Genome Institute.
                                                                                                                                     Hominidae; Homo.

1 (bases 1 to 209844)

DOE Joint Genome Institute
                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                209844 bp DNA
Homo sapiens chromosome 19 clone CTB-33G10,
AC011495
DOE Joint Genome Institute and Stanford Human Genome Center
                                                                                                        Unpublished
                                                                                                                          Direct Submission
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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27583. .27885
/rpt family="AluSx"
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Submitted (26-NOV-2000) DOE Joint Genome Institute, 2
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 209844)
DOE Joint Genome Institute and Stanford Human Genome
                                                                                                                                                                                                     173556 bp
Homo sapiens chromosome 2 clone
SEQUENCE, 21 unordered pieces.
ACO74388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-JUL-2002) DOE Joint Genome Institute, 2800 M. Drive, Walnut Creek, CA 94598, USA On Jul 14, 2002 this sequence version replaced gi:15281207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-AUG-2001) DOE Joint Genome Institute, Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: Phrap Quality >=40 99.9% of Sequence; Estimated Total Number of Errors is 0.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Finishing Completed at Stanford Human www-shgc.stanford.edu
2 (bases 1 to 173556) Waterston, R.H.
                                          1 (bases 1 to 173556)
Waterston,R.H.
The sequence of Homo sapiens
                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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                               Unpublished
                                                                                             Hominidae; Homo.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
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Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 158826 bases at least Q40
Consensus quality: 15338 bases at least Q30
Consensus quality: 15564 bases at least Q20
Insert size: 166000; agarose-fp
Insert size: 171556; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (30-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Aug 4, 2000 this sequence version replaced gi:9587428.
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Center code: WUGSC
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Quality coverage: 4.61 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/estimated_length=unknown
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/note="assembly_name:Contig26"
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20451. .25976
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20351. .20450
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|5824. .15923
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L1727. .15823
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L1627. .11726
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                1795
                                                                                                                                                                                                1675
                                                                                                                                                                                                                                                               1615
                                                                                                                            1735 CAGGAGTGGTGGCACACCTGTAATTCCAGCTACTCAGGAGGATGAGGCAGGAGAATCA 1794
                                320
                                                                                               261
                                                                                                                                                               201
                                                                                                                                                                                                                           81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                             CTTGAACCCAGGAGGCGGAGGTTGCAATAAGCCGAGATTGCGCCACTGCGAGACTCTGTC 185
ТСАЛАЛЛАТЛАЛАТАЛАЛАТАЛАЛАТЛАЛАЛАДССАСТ 1894
                                                                                                                                                            TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                            TCAAAAACAACAAAAAAAAAAAAAACCATAAGACATT 359
                                                                                             TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAG-CAGAGTGAGACKCCGTC 319
                                                                                                                                                                                            TCGAGACCAGCCTGGCCAACATGGCGAAACCCCTGTCTCTACTAAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                             AGGCCTGTAATCCCAGTACTTTGGGAGGCCAAGGTGGGCGGATCACTTGAGGTCAGGAGT 167
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87827. .87926
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115285. .13270
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132704 132803
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132804 154064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99072. .99171
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15185. .115284
estimated_length=unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .11518
                                                                                                                                                                                                                                                                                                                          Score 157.2; DB 1
Pred. No. 1.2e-42;
1; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                         DB 12;
                                                                                                                                                                                                                                                                                                                            69;
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                         Length 173556;
                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                          Gaps
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REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE RESULT 25 AL162739/c COMMENT DEFINITION JOURNAL ORGANISM Human DNA sequence from clone RP5-1155K23 on chromosome 1p31.3-32.3 Contains a Down syndrome critical region gene 5 (DSCR5) pseudogene, a ribosomal protein S15a (RP515A) pseudogene, a novel gene (FLJ10884), a ribosomal protein L36 (RP136) pseudogene, a novel gene end of a novel gene, complete sequence. Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 25, 2002 this sequence version replaced gi:16973818.
The following abbreviations are used to associate primary accession AL162739.24 GI:21211651 HTG; DSCR5; FLJ10884; RPL36; RPS15A. Homo sapiens (human) Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutharia; Euarchontoglires; Primates; Catarrhini; Homo sapiens Direct Submission Hominidae; Homo. (bases 1 to 84001)

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FEATURES
                                                                                                                                                                                            mRNA
                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
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Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/DIT
RP5-1155K23 is from the library RPCI-5 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VECTOR: pCYPAC2
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Tr.Q8UW22 Tr.Q962R3 Tr.Q9IA74"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                             /locus_tag="RP5-1155K23.3-001"
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'mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="match: proteins: Sw:P57054 Tr:AAP35702 Tr:Q9JHG1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tocus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .855. .22259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .84001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .22259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _tag="RP5-1155K23.1-001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dGTP big dye
                                                                                                                                                                                               .38969,41116.
1 Em:AI624743.
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                                                                                                                                                                                                                                                                                                                                                                                                            Sw:Q90YQ8
                                                                                                                                                                                                                                                                             .43661)
                                                                                                                                                                                               .43661)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
        mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyA_site
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RÉFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 26
AÇ025599/c
                                                                                                                                                                                                                                                                    CEYWORDS
                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                      ERSION
                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                       CESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG
                                                                                                                                                                                                                                                                                               Homo sapiens chromosome 8,
AC025599
AC025599.8 GI:18464214
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                        Homo sapiens
                                                                                                           Hominidae;
(bases 1 to 158330)
itrren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAAAAAAAAAAAAGAATAATAC 57459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   АААСААСААСААААААСААААААС 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATTG-----TGCCATTGCACGCTAGCCTGGGCAACAAGAGTGAAACTCTATCTCAA 57484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGTGGTGGTGCACGCCTATAATCCCCAGCTACTCGGGAGGCAGAGGTTGCAGTGAGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTACTAAAAATACAAAATTAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTGTAATCCCAGCACTTTGGGAGGCCAAGCTGGGCAGATCACCTGAGGTCAGGAGTTTG
                                                                                                                                                                                                                                   sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="novel protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (AL139343 9:30881 39966), complement (AL139343 9:22536 24419), complement (AL139343 9:22536 2491), complement (AL139343 9:10810 17937), complement (AL139343 9:17619 17837), complement (AL139343 9:16064 16151), complement (AL139343 9:12424 12643), complement (AL139343 9:12424 12643), complement (AL139343 9:2399 2541),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      match: cDNAs: Em:AK096259.1 Em:BC033147.1" join(complement(AL139343.9:68437. .68745),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Iocus tag="RP5-1155K23.5-001"
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                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 157; DB 5
Pred. No. 1e-42;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         158330 bp
                                                                                                                                                                                                                                                                                                                                                           clone RP11-508K19, complete sequence.
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   clone="RP11-508K19"
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Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Sentos, R., Schauer, S., Severy, P., Spencer, B., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Venna, G., 7since, A., Milson, B., Mu, X., Wyman, D., Ye, W.J., Venna, G., 7since, A., Milson, B., Mu, X., Wyman, D., Ye, W.J., Venna, G., 7since, A., Milson, B., Mu, X., Wyman, D., Ye, W.J., Venna, G., 7since, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Venna, G., 7since, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Venna, G., 7since, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Venna, G., 7since, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Venna, G., 7since, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Venna, G., 7since, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Venna, G., 7since, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Venna, G., 7since, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Venna, G., 7since, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Venna, G., 7since, 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Anderson, S., Baldwin, C., Barna, N., Bastien, V., Beda, F. Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collymore, A., Cooke, F., Dalar, K., Dewar, K., Diaz, Collymore, A., Cooke, F., Dalar, Cooke, F., Dal
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Center clone name: 508_K_19
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mol_type="genomic DNA"
chromosome="8"
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/rpt_family="Alusx"
complement(16455. 16545)
/rpt_family="MER69"
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/rpt_family="L2"
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/rpt_family="L2"
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13266 .13273
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complement(12437. .13784)
/rpt famil. ""
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complement(13785. .13893)
/rpt_family="L1PR1"
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complement(12288. .124
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complement(15921. .162
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/rpt_family="AluSx"
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complement(11709. .120
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                                                                                                                             /rpt_family="L1PB3"
complement(13895. .14264)
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1222. .11285
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          195070 bp DNA linear H
Homo sapiens chromosome 3 clone RP11-463G10, WORKING
SEQUENCE, 23 unordered pieces.
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complement(35666. .36486)
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/rpt_family="MLTIC"
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/rpt_family="MSTB"
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/rpt_family="L1PA7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 29, 2000 this sequence version replaced gi:11024742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Arc, J.R., Banks, T., Barbaria, J., Bentton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burcet, C., Burcell, K.L., Byrd, N.C., Carron, T.F., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., Davila, M.D., Davis, C., Coyle, M.D., Davis, C., C
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Center clone Hause.

Center Clone Hause.

Sequencing vector: M13; L08821

Chemistry: Dye-terminator Big Dye: 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 160818 bases at least Q40

Consensus quality: 177694 bases at least Q20

Consensus quality: 184433 bases at least Q20

Estimated insert size: 185987; sum-of-contigs estimation

Estimated insert size: 185987; sum-of-contigs estimation
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
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Center clone name: RP11-463G10
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/estimated 63726. .63

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/db_xref="taxon:9606" organism="Homo sapiens"

clone="RP11-463G10"

53726. .63825 /estimated_length=unknown 78735. .78834

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                             AL353145.4 GI:9796994
HTG; HTGS_PHASE1; HTGS_CANCELLED
                                                                             AL353145 111372 bp
Homo sapiens chromosome 1 clone
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                                                                  unordered pieces.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                   AGGAGCCGGAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGA
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          sapiens
                       sapiens (human)
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108564. .108663
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95254. .95353
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147338. .147437
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139483. .139582
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Pred. No. 1.8e-42;
L; Mismatches 83
                                                                            DNA linear HTG 10-JUL-2001 RP4-633K13 map p34.3-36.11, 9
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CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 12, 2000 this sequence version replaced gi:9213061.
                                                                                                                       Direct Submission Submitted (09-JUL-2001) Sanger Centre,
                                                                                                                                                                                                                            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Chemistry: Dye-terminator ABI; 1% of reads
Chemistry: Dye-terminator Big Dye; 74% of reads
Chemistry: Dye-terminator ET-amersham; 24% of reads
Chemistry: Doe-terminator ET-amersham; 24% of reads Consensus
quality: 10538 bases at least Q40
Consensus quality: 107404 bases at least Q30
Consensus quality: 108616 bases at least Q20
Insert size: 110572; sum-of-contigs
Insert size: 124558; 7.7% error; agarose-fp
Quality coverage: 3.70x in Q20 bases; sum-of-contigs Quality Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 1 coverage: 3.47x in Q20 bases; agarose-fp Contact: humquery@sanger.ac.uk Web site: http://www.sanger.ac.uk Summary Statistics name: dJ633K13 Project Information 100% of reads

NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1: contig of 3034 bp in length
2: gap of 100 bp
3: contig of 9274 bp in length
3: gap of 100 bp
7: contig of 19409 bp in length
7: gap of 100 bp
1: contig of 17784 bp in length
1: gap of 100 bp
1: gap of 100 bp
1: gap of 100 bp
3: contig of 25192 bp in length contig of 12632 bp in length gap of 100 bp contig of 5471 bp in length contig of 5289 bp in length gap of 100 bp contig of 12487 bp in length gap of 100 bp gap of 100 bp of 12632 bp in length

""" fragment:01234 1. 111372 /organism="Homo sapiens" /organism="Genomic DNA" /mol_type="genomic DN /db_xref="taxon:9606" /chromosome="1" note="assembly_fragment:01010 ragment_chain:1" note="assembly_fragment:00063 ragment_chain:l" map="p34.3-36.11" clone="RP4-633K13" clone_lib="RPCI-4" 12408

COMMENT

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                                                                                  Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F., Boukhigalter,B., Brown,A., Burkett,G., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J., Ferreira,P., Fitzhugh, W., Forrest,C., Gage,D., Galagan,J., Gardt,G., Horton,L., Gardyna,S., Grant,G., Haggos,B., Heaford,A., Horton,L., Gardyna,S., Grant,G., Hogos,B., Heaford,A., Horton,L., Lin,G., Locke,K., Lianders,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K., Lianders,T., Lia
                                                                                                                                                                                                                                                                                                                                                                                                            Birren,B., Linton,L., Nusbaum,
Homo sapiens, clone RP11-28012
Unpublished
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Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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105902. .111372
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fragment_chain:3"
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ragment_chain:3"
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fragment_chain:2"
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/note="assembly
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chain:2"
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------ Genome Center
Center: Whitehead Institute/ MIT Center for Genom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (27-JAN-2000) Whitehead Institute/MIT Center for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.
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Center clone name: 28 0 12

Center clone name: 28 0 12

Center clone name: 28 0 12

Sequencing vector: M13; M7781.5; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 132159 bases at least Q40

Consensus quality: 141146 bases at least Q30

Consensus quality: 144793 bases at least Q20

Insert size: 157000; agarose-fp

Insert size: 157000; agarose-fp

Quality coverage: 3.1 in Q20 bases; sum-of-contigs

Quality coverage: 3.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WIBR Web site: http://www-seq.wi.mit.edu
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gap of 100 bp
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contig of 1889 bp in length
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contig of 1479 bp in length
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of 4000 bp
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12137. .13936
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109294: contrig of 11156 bp in length

109394: gap of 100 bp

123250: contrig of 13856 bp in length

123350: gap of 100 bp

134759: gap of 1100 bp

150934: contrig of 16175 bp in length.
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contig of 6392 bp in length
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g of 5135 bp in :
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SOURCE
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Best Local Similarity
Matches 201; Conserv
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2 (bases 1 to 163521)
Waterston,R.H.
Direct Submission
Submitted (24-JAN-2002) Genome Sequencing Center, Washington
                                                                                         1 (bases 1 to 163521)
Waterston, R.H.
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                        HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                    SEQUENCE, 4 unordered p. AC108040 GI:18425316 AC108040.2 GI:18425316
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                                                          The sequence of Homo sapiens 
Unpublished
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73.1%;
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Pred. No. 1.8e-42;
0; Mismatches 74;
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RP11-210010, WORKING DRAFT
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37 AAATATTAATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCTGTAATCCCAG 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 189000; agarose-fp
Insert size: 163221; sum-of-contigs
Quality coverage: 8.88 in Q20 bases; agarose-fp
Quality coverage: 8.85 in Q20 bases; sum-of-contigs
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On Jan 30, 2002 this sequence version replaced gi:18308830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: M13; 0% Sequencing vector: plasmid; 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces
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89085
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1565
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/estimated_length=unknown
112803. 163521
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89085. .112702
                                                                                                                                                                                                                                                                                                                                   vector_side:left"
88985. .89084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_name:Contig25
clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="4"
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1664: gap of unknown length
88984: contig of 87320 bp in length
89084: gap of unknown length
112702: contig of 23618 bp in length
112802: gap of unknown length
163521: contig of 50719 bp in length.
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71.4%;
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                                               1; Mismatches
                                                                   Score 156.6; DB 12;
Pred. No. 1.9e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-MAR-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA 3 (Dases 1 to 196773) Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and
                                                                                                                                                                                                                                                                                                                                                                         Submitted (29-JAN-2003) Genome Center, University of Washington, Box 352145, Seattle, MA 98195, USA On Jan 29, 2003 this sequence version replaced gi:19310299.
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Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
Direct Submission
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1 (bases 1 to 196773)

Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A.,
Saenphimmachak,C., Buckley,D., Kibukawa,M.,
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Direct Submission
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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HTG.
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Sequencing vector: unknown; 3% of reads Sequencing vector: plasmid; 97% of reads Chemistry: Dye-terminator ET; 94% of reads Chemistry: Dye-terminator Big Dye; 6% of reads Chemistry: Dye-terminator Big Dye; 6% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 196438 bases at least Q40 Consensus quality: 196751 bases at least Q30 Consensus quality: 196772 bases at least Q20 Insert size: 196773; sum-of-contigs
                                                                                                                                                                                         Center project name: chr-3
Center clone name: RP11-755810 (bc0671)
------ Summary Statistics
                                                                                                                                                                                                                                                                                    Contact: uwgchtgs@u.washington.edu
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Raymond, C. and
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1971 1982 2797 2775 5594 5591 591 591 591 591 591 591 591 591 59	2876 2910 2548 2558 1067	2510 2531 889 873 4466 4431	9289 6793 6788 3014	2522 2531 5764 5726 6707 6693	6457 881 873	1386 1035 1032 1619	519 <800 3752 3826 5493 5591	7000 1000 1000 1000 1000 1000 1000 1000	2241 449 <800 13590	4995 4998 512 <800 12782 12807	6 <800 6382 6490 2067 2051	8696 8856 3845 3999 10997 10643		SeqDerMap FngrPrnt SeqDerMap FngrPrnt SeqDerMap FngrPrnt	ECORI HindIII BglII	between the experimental and predicted values. Uniquely ordered	small tragments below a variable cutoff (approximatery 400-000 pp) are not resolved in the fingerprint and hence do not appear in the table there are no ejectificant remaining discrepancing	The electronically-digested sequence consists or both insert and vector, in order to accurately represent the entire circular BAC.	fragments with sequence-predicted fragments is given below.	sequence validation: This sequence has been validated by Multiple Complete Digest finormatistic Comparison of the experimentally derived digest	subclone; and the assembly was confirmed by restriction digest.	problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13	quality >= 30); an attempt was made to resolve all sequencing	This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an	of this entry's ASN.1 file.	Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part	Quality levels above 40 are expected to have less than 1 error in 10,000 bp.	All manually edited bases have reduced to quality zero.	Sequence Quality Assessment: This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.		3': RP11-680P23 (UWGC:bc0527) AC092418, 11308-bp overlap	לייין בייי לייינים אמלי יייזא דוו לבט אמסכט, סמווייטר כטורידאָס לייין ביייי לייינים אמלים בייייים לייין אנט אמסכט, סמווייטר כטורידאָס	Onality coverage: 8.4x in O20 bases: sum-of-contigs
Ouery Match 39.2%; Score 156.6; Le 5; Le 19.11 1907/3; Best Local Similarity 71.4%; Pred. No. 2.1e-42; Matches 222; Conservative 1; Mismatches 80; Indels 8; Gaps Oy 37 AAATATTAATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCTGTAATCCCAG 9	10 18. CONTA 156 A. DR S.	/chromosome="3" /clone="RP11-75B10" /clone lib="RPCI human BAC library 11"	/organism="Homo Belouis" /db_xref="taxon:9606" /db_xref="taxon:9606"	FEATURES LOCATION/QUALIFIERS Source 1, .19673			22128 22660 	3328 3518	 8874 8921	2063	967 4016	 <800 17962 1	328 <800 4499 4387 	NH	6490	2800 6707	15091 1088 1032		20004	<800 5370	Д.		18633	10/10 1	2600 14021 14200 2027 7607 7507 2104	4390 341 6800 324	2004 2300 2300 5324 2000 5321 2000 5324	2604 2918 2906 266		16576 5371	1886 1862 846	3357 540 7800 4314	1196 1166 552 <800 6602 6693

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Consensus quality: 92975 bases at least Q40
Consensus quality: 98251 bases at least Q30
Consensus quality: 100181 bases at least Q30
Estimated insert size: 106000; pulse field gel estimation
Quality coverage: 5.46 in Q20 bases; pulse field gel estimation
Quality coverage: 5.69 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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Center: Joint Genome Institute
Center Code: JGI
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Submitted (04-DEC-1999) Production Sequencing Facility, DOE Joint Sequence Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On May 6, 2000 this sequence version replaced gi:7710241.
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Center clone name: CIT-HSPC_285M15
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Homo sapiens chromosome 5 clone
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC016552.5 GI:7711562
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CTC-285M15, WORKING DRAFT
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DRAFT SEQUENCE,
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ORGANISM
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AC008499.8
HTG.
                     Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9459
3 (bases 1 to 244525)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (06-DEC-2001) DOE Joint Genome Institute,
                                                                                                         2 (bases 1 to 244525)
DOE Joint Genome Institute.
                                                                                                                                                                      1 (bases 1 to 244525)
DOE Joint Genome Institute
                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                  Homo sapiens chromosome
                                                                                                                                                       Direct Submission
                                                                                                                                                                                                     Hominidae; Homo
                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                               AC008499
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                                                                                                                                                                                                                                                                                                                                                                                                                                CTCAAAAAACAAAACAAAACAAAAAAAAAAGTAATAAGTGCTTG 71406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCTTĠAACCCAĠGAGĠTĠGAĠCCTGCAGCCTG-GGCAACAGAGTGAGACTCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCAAAAACAACAACAAAAAAACCAAAAAAACCATAAGACATTG
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/clone_lib="CalTech human BAC library C"
63902._.64001
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01205. .101304
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/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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64001: gap of unknown length
92415: contig of 28414 bp in length
92515: gap of unknown length
101204: contig of 8689 bp in length
101304: gap of unknown length
102008: contig of 704 bp in length.
                                                                                                                                                                                                                                                                                                   GI:18376856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length=unknown
                                                                                                                                                                                                                                                                                                                               244525 bp DNA linear
Ne 5 clone CTC-438O3, complete
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Pred. No. 1.8e-42;
L; Mismatches 62
                                                                                                                                                                       and Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62;
                                                                                                                                                                       Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                sequence.
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                                                         , DOE Joint
A 94598, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
2 (bases 1 to 88848)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collynore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
                                                                                                                                                                                                                                                              1 (bases 1 to 88848)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone CTD-2314M10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (26-JAN-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jan 26, 2002 this sequence version replaced gi:17386226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 244525)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens chromosome AC107377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: Phrap Quality >=40 99.7% of Sequence; Estimated Total Number of Errors is 0.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 (bases 1 to 244525)

DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC107377.4 GI:20377031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Finishing Completed at Stanford Human Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGGTGTGGGGGCACACGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGCAGAAT 86622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGCCTGTAATCCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCTTGAACCCAGGAGGTGGAGCCTGCACTCCAGCCTG-GGCAACAGAGTGAGACTCCGT 86563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCAAAAACAACAACAAAAAAACAAAAAAAACCATAAGACATTG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Produced by DOE Joint Genome Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="CTC-43803"
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76.6%;

    Mismatches

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Pred. No. 2.7e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88848 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA linear PRI 01-MAY-2002 CTD-2314M10, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
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MecLean C. Macdonald D. Major J. Levine, R., Liu G. MecCenthy, M., MecCenald D. Major J., Marquis, M. Matthews, C., MecCenathy, M., MecCenan, K., Mepheeters, R., Meldrin, J., Meness L., Macdonald, D., Major J., Marquis, M., Matthews, C., MecCenar, M., Meldrin, J., Meness L., Minbowa, T., Meness L., Maylor, J., Sanyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Neil, D., O'Neil, D., Mercenar, G.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Neil, D., Mercenar, G.H., O'Connor, T., O'Donnell, P., O'Neil, D., Mercenar, G.H., O'Reil, D., Mercenar, G.H., O'Reil, D., Mercenar, G.H., O'Reil, D., Mercenar, G.H., O'Reil, D., Mercenar, G.H., Mercenar, G.H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L21459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center clone name: 2314_M_10
                                                                                                                                                                                                                        /rpt_family="Alusc"
complement(9022. .932A)
/rpt_family=""
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/rpt_family="AluSx"
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complement(5101.
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complement(1891.
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complement(98. .394)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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    'rpt_family="AluJo"
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family="FRAM"
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                      family="AluY"
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family="MIR"
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Matches 212; Conserv
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AC172796.2 G1:86203525
HTGS_PHASE2; HTGS_DRAFT.
Callicebus moloch (DusKy titi)
Callicebus moloch (Company Caraniata; Vertebrata; Euteleostomi; Callicebus moloch (Company Caraniata; Vertebrata; Euteleostomi; Callicebus, Euarchontoglires; Primates; Platyrrhini; Cebidae; Callicebinae; Callicebus.

1 (bases 1 to 182725)
Antonellis, A., Bass, D., Benjamin, B., Bera, J., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooke, S., Chu, G., Coleman, H., Franks, S., Fuksenko, T., Gestole, M., Greene, A., Guan, X., Gupta, J.,
                                                                                                                                                                                                         AC172796
Callicebus
                                                                                                                                                                                                                                                                                                                                                                                                                                TGGGTGTGGTGGGGGGCGGTAATCCCAGCTACTCAGGAGGCGGAGGTTGCAGTGAGC
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                                                                                                                                                                                                                                                                                                                          CAAAAACAACAACAAAAAAACAAAAAAAACCATAAGACATTGTCC
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/rpt_family="AluSx"
19095...19142
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/rpt_family="Alusx"
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complement(14478. .14608)
/rpt_family="FLAM_C"
14917. .14938
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moloch clone LB5-41K3,
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Pred. No. 2.7e-42;
0; Mismatches 62
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* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 22543: contig of 22543 bp in length

* 22544 22643: gap of unknown length

* 22644 31875: contig of 9232 bp in length

* 31876 31975: gap of unknown length

* 31976 122998: contig of 91023 bp in length

* 123099 123098: gap of unknown length

* 123099 1336487: contig of 13389 bp in length

* 136488 136587: gap of unknown length

* 136488 136587: gap of unknown length

* 136588 139369: contig of 2782 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is generally based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (31-JAN-2006) NIH Intramural Sequencing Center, 99 Fishers Lane, Rockville, MD 20852, USA On Jan 31, 2006 this sequence version replaced gi:82617757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-NOV-2005) NIH Intramural Sequencing Center, 5625 Fishers Lane, Rockville, MD 20852, USA
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Green, E.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. Gaps between the contigs are represented as uns of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 182725)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 179767 bases at least Q40
Consensus quality: 180990 bases at least Q30
Consensus quality: 181586 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: mrn
Center clone name: 041K03
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Contact: nisc_zoo@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality coverage: 9.44x in Q20 bases; agarose-fp Quality coverage: 11.11x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert size: 214000; agarose-fp
Insert size: 181925; sum-of-contigs
Quality coverage: 9.44x in Q20 bases; agarose-fp
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    Summary Statistics

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Best Local Similarity
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                                                                  ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
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                                                                                                                                    Conservative
                                                                                                                                                                                                                   /note="assembly_fragment
clone_end:SP6
vector_side:right"
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/estimated_length=unknown
123099. .136487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="clone overlaps with GenBank Accession Number AC174418 clone LB5-285I22 (center project name mrm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment
missing T7 clone end on 5' end of insert'
                                                                                                                                                                                                                                                                        179902. .18272
                                                                                                                                                                                                                                                                                                                                                                                                     , cascimated length=unknown
148709. .157275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Callicebus m
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /estimated_length=unknown
139470. .148608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment"
136488. .136587
/estimated_length=unknown
136588. .139369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="clone overlaps with GenBank Accession Number
AC172795 clone LB5-290P9 (center project name mro)"
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31976. .122998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="LB5"
/note="BAC resource: http://bacpac.chori.org/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="LB5-41K3"
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                                                                                                                                                                                                                                                                                                                                       57376. .179801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="assembly_fragment"
39370. .139469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_fragment"
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148608: contig of 9139 bp in length
148708: gap of unknown length
157275: contig of 8567 bp in length
157375: gap of unknown length
179801: contig of 22426 bp in length
179901: gap of unknown length
182725: contig of 2824 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                              .148708
                                                                                                                                                                                                                                                                                                                                                         _length=unknown
                                                                                                                                  Score 155.8; DB 12;
Pred. No. 3.9e-42;
1; Mismatches 83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (30-NOV-1998) Department of Molecular Biotechnology, Boy 357730 University of Washington, Seattle, Washington 98195, USA Sequencing methodology: high redundancy shotgun using plasmids. Interspersed Repeats were identified with RepeatMasker (available from http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216387 bp DNA linear PRI 23-DEC-1998 Homo Bapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and 8171 gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rowen,L., Madan,A., Qin,S., Abbasi,N., Dors,M., Madan,A., Dickhoff,R., Shaffer,T., James,R., Lar Complete sequence of the gene for presentin 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lb="P. deJong R complement (262. 556) /rpt family="AluJo" 750. 1064
                                                                                                                                                                                                                                                                                                                                                                       poin(<1465. .1522,5979. .6139,14890. .15075,17363. .17416, 17650. .17733,21177. .21463,23822. .24044,24159. .24248, 25789. .25862,27305. .27455,28794. .29118,29491. .29765, 30115. .30213,32250. .32297,37674. .>37766)
                                                                                 join(<1465...1522,5979...6139,14890...15075,17363...17416, 17650...17733,21177...21463,23822...24044,24159...24248, 25789...25862,27305...27455,28794...29118,29415...29765, 30115...30213,33250...32297,37674...37786)
//note="unknown; intron-exon boundaries defined by ESTs A1247672, AA6777613, AA677761, T40389, AA74425, AA910441, AA170655, and cDNA in 140392; the sequence in 140392 begins at 28812; the exons from 21177-21463 and 23822-24044 contains a repeat; only 1 EST, 740380 matches the exon 5 contains and 23822-24044 contains a repeat; only 1 EST, 740380 matches the exon 5 contains and 23822-24044 contains a repeat; only 1 EST, 740380 matches the exon 5 contains and 23822-24044 contains a repeat; only 1 EST, 740380 matches the exon 5 contains and 23822-24044 contains a repeat; only 1 EST, 740380 matches the exon 5 contains and 23822-24044 contains a repeat; only 1 EST, 740380 matches the exon 5 contains and 23822-24044 contains a repeat; only 1 EST, 740380 matches the exon 5 contains and 23822-24044 contains a repeat; only 1 EST, 740380 matches the exon 5 contains and 23822-24044 contains a repeat; only 1 EST, 740380 matches the exon 5 contains and 23822-24044 contains a repeat; only 1 EST, 740380 matches the exon 5 contains and 23822-24044 contains a repeat.
T40389 matches the exon from 21177-21463; since several ESTs end in the beginning of this exon, and several 5' ESTs start at the end of this exon, it is possible that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"
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Lasky, S. and Hood, L.
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complement(2523. .2820)
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12447. .12450
                                                                                                                      complement (10714...10844)
/rpt_family="FLAM_C"
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complement(12658. .12788)
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complement(10572. .1
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complement(3956..4
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GEKKLLVKVDAKTKAQLDEWKAKKKASNGNARPETVINDDEEALDEETKRRDQMIKGA
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Tement("1777"
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complement(21557.
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complement(22333. .22)
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family="AluSg"
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family="POLY_A"
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7. .13597
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                                                                                                                                                                                                                                                                                                                                                         AL Submitted (13.MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 2, 2002 this sequence version replaced gi:23393869. On Cot 2, 2002 this sequence version replaced gi:23393869. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/Hgp/ChrX
RP13-44K19 is from the library RPCI-13.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human DNA sequence from clone RP13-444K19 on chromosome X Contains a mitochondrial ribosomal protein S18C (MRPS18C) pseudogene, the 3' end of the gene for a novel protein similar to PHD finger protein 2 PHF2 and a CpG island, complete sequence.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL732374.14 GI:23476649
HTG; CpG island; MRPS18C; PHF2.
                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                   Center: Wellcome Trust Sanger Institute Center code: SC
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 224187)
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                                                                                                                                                                                                                                                                                                                                         //www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.0%;
                                                                                                                                                                                                                                                                                         Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 155.8; DB 5
Pred. No. 4.2e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join (Complement (AL589872.9:883.971),

complement (298051.7:6109.6298),

complement (208423.208508), complement (207924.208032),

complement (208423.208508), complement (202260.202401),

complement (20326.203486), complement (196787.196949),

complement (188260.188347), complement (187820.186949),

complement (188260.188347), complement (187820.187926),

complement (188535.185626), complement (181388.181447),

complement (179266.179568), complement (172743.178504),

complement (173431.173609), complement (172743.172828),

complement (188509.148604), complement (170579.170892),

complement (125845.126181), complement (12347.124911))

//gene="piff8"
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                                                                                                                                                                                                                                                                                                                                                                    complement (join(123382: .123724,124827: .124911, 125845: .126181,129799: .129708,148509: .148604, 170579: .170892,171481: .171614,172743: .172828, 173431: .173609,178401: .178504,179266: .179568, 181358: .181447,185535: .185626,187920: .189347,196787: .196949,200042: .200228, 202260: .202401,203326: .203486,207924: .>207927), /gene="PHF8"
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173431. 173609,178401. 178504,179266. 179568,
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188260. 188347,196787. 1185626,207924. >207927,
202260. 120228,1203326. 203486,207924. >207927,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (208423 . 208508), complement (207924 . 208032), complement (203326 . 203486), complement (202260 . 202401), complement (20042 . 203486), complement (19678 . 196949), complement (19678 . 196949), complement (188260 . 188347), complement (187820 . 187926), complement (185535 . 185626), complement (18158 . 181447), complement (179266 . 179568), complement (178401 . 178504), complement (173431 . 173609), complement (170579 . 170828), complement (171481 . 171614), complement (170579 . 170828), complement (148509 . 148604), complement (129799 . 129908), complement (125845 . 126181), complement (122347 . 124911))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_lib="RPCI-13.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the rare occasion of the clone being a YAC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           locus_tag="RP13-444K19.2-001"
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b_xref="taxon:9606"
lone="RP13-444K19"
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/db xref="UniProtKB/TrEMBL:05VUJ4"
/db xref="Uni
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complement (208423. 208508).complement (202260. 2000).

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complement (171481. 171614).complement (172799). 1700.

complement (172845. 126181).complement (129799. 1700).

complement (125845. 126181).complement (124823. 126181).complement (124823. 126181).
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DLFREFNFETICWYVGKHILDIFRGLERNRHPASYLVHGGKALNLAFRAWTRKEALF
DHEDEIPETVRTVQLIKDLAREIRLVEDIFQQNVGKYSNIFGLQRIFPAGSIFLTRALF
HSTSVSMSRLSLPSKNGSKKKGLKPKELFKKAEKKGKESSALGPAGQLSYNLMDTYSH
QALKYGSFQKAKFNITGACLMDSDDDSPDLDLDGNGSFLALLMSGSTKRVKSLSKSR
RTKIAKKVDKARLMAEQVMEDEFDLDSDDENLDGNGSFKALTLIIRPKFPRKLFKARR
PCSDDNRVREPGETVEFIEEDYTTDEDBNDEGVEKLGNGSGAGGILDLLKASRQVGFB
DYAALTEAPASPSTQEAIQGMLCMANLQSSSSPATSSLQAWWTGGQDRSSGSSSGGL
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/note="match: proteins: BAC65729 Q9UPP1"
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.181447),
.178504),
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ACCESSION
VERSION
KEYWORDS
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TITLE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                  Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
On Nov 7, 1999 this sequence version replaced gi:6165363.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: RMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
was generated from part of bacterial clone contigs of human
                                                                                                                                     chromosome 6, constructed by the Sanger Centre Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human DNA sequence from clone RP1-193N13 on chromosome 6q21-22.31 Contains the 5' end of the MANIA1 gene for mannosidase, alpha, class 1A, member 1 (Man9-mannosidase (MAN9), HUMM9). Contains a CpG
                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 122961)
  Center:
                                            VECTOR: PCYPAC2
                                                                  Pieter de Jong. For further deta
http://www.chori.org/bacpac/home
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mannosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALO78600.15 GI:6273536
HTG; CpG island; HUMM9; MAN1A1; MAN9; Man9-mannosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSJ193N13
                                                                                                                 RP1-193N13 is from the library RPCI-1 constructed by the group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Wellcome Trust Sange
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KLAQQELQKAQKKKYIKKKEPLLKEVEQPRPQDSNLSLTVPAPTVAATPQLVTSSSPLP
PPEPKQEALSGSLADHEYTARPNAFGMAQANRSTTPMAPGVFLTQRRPSVGSQSNQAG
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74.1%;
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Pred. No. 5e-42;
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Sanger Institute
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(complement(51672...52274), complement
complement(5197...5312),
complement(ALO22722.1:132996...133076),
complement(ALO22722.1:190573...90667),
complement(ALO22722.1:47072...47195),
complement(ALO22722.1:47072...43660),
complement(ALO22722.1:36090...36205),
complement(ALO22722.1:36090...36205),
complement(ALO22722.1:31977...32196),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (ALO22722 1:90573 90667), complement (ALO22722 1:47072 47195), complement (ALO22722 1:43607 43660), complement (ALO22722 1:43567 43660), complement (ALO22722 1:35090 36205), complement (ALO22722 1:31977 32196), complement (ALO22722 1:30718 30890), complement (ALO22722 1:23625 22740), complement (ALO22722 1:25625 22740), complement (ALO22722 1:25625 22740)
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AL135738 AL673800 AU119410 AU135696 AV650705 AV689108
AV701374 BE003222 BE815845 BE877565 BC428373 BC548683
BI441201 BI964041 BI964247 BM538709 BM806736 BM933828
match: CDNAs: AF027156 AK025599 U03457 U03458 U04299
U04301 X74837 Y12503"
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complement (10105.
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                                                                                                                                                                                                                                                                                                                                                                                  /gene="MAN1A1"
/locus_tag="RP3-354N19.2-001"
/standard_name="0TTHUMP00000017107"
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/clone="RP1-193N13"
/clone_lib="RPCI-1"
                                                                                                                                             /proteIn id="CAB75695.2"
/db_xref="GI:56203652"
/db_xref="GOA:P33908"
/db_xref="HGNC:6821"
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/note="match: ESTs: AA317167 /
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join(complement(5197. .
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mol_type="genomic DNA"
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933908 p39098 p45700 p45701 p53624 p53625 Q18788 Q9NR3
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?LRDKAPFRGLPPVDFVPPIGVESREPADAAIREKRAKIKEMMKHAWNNYKGYAWGLN

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JOURNAL
PUBMED
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                                                                                                         AUTHORS
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Best Local Simi
Matches 210;
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MO 63108, US
5 (bases 1 1
Waterston, R.
                                                  Direct Submission
Submitted (24-MAR-1999) Genome
University School of Medicine,
                                                                                                       4 (bases 1 to Waterston, R.H.
                                                                                                                                                            Submitted (12-JUN-1998) Genome University School of Medicine,
                                                                                                                                                                                                                 3 (bases 1 to 126462) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                           Toward a complete human genome Genome Res. 8 (11), 1097-1108
                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 126462)
Sulston, J.E. and Waterston, R.
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                                 USA
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SVFEVNI RFVGGLLSAYYLSGEBI FRKKAVBLGVKLLFAFHTESGI PRALLNMKSGIS
RNWFWASGGSS I LAEFGTLHLEFMHLSHLSGNB I FAEKVMNI FTVLNKLEKPQGLYBN
YLNPSSGQWGQHHVSVGGLGDSFYEYLLKAWLMSDKTDLEAKKMYFDAVQA I ETHLI R
KSSGGLTY I AEWKGGLLEHKWGHLTCFAGGWFALGADAAPEGKAQHYLEIGABI TATC
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WAWBAVEALENHCRNGGYSGLRDVYLLHESYDDVQOSFFLAETLKYLYLI FSDDDLL
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Pred. No. 4.4e
1; Mismatches
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(1998)
                                                    Sequencing (
                                                                                                                                                            Sequencing Center, Washington 4444 Forest Park Parkway, St.
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t Park Parkway, St.
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Submitted (28-JUL-1999)
University, 4444 Forest
6 (bases 1 to 126462)
                                                                                                                                                  University, 4444 Forest Park Avenue, St. Louis, Missouri 6
On Mar 24, 1999 this sequence version replaced gi:3213121.
                                                                                                                                                                                              Submitted (21-DEC-1999)
                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                        Waterston, R.
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_DJ0747G18
                                                              Web site: http://genome.wustl.
                                                                                      Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                          21-DEC-1999) Department of Genetics, Washington 4444 Forest Park Avenue, St. Louis, Missouri 6
                                                                                                                                  -- Genome Center
                                                                                                                                                                                                                                                                              Department of Genetics, Park Avenue, St. Louis,
                                                                edu/gsc
                                                                                                                                                                                                                                                                                Washington
Missouri 63108,
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clone se one. It may be shorter because we only sequence overlapping one sections once, or longer because we provide a small over neighboring data submissions. This sequence may not represent the entire insert of this overlap

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc MAPPING INFORMATION: and

This clone was derived from human PAC library RPCI-4, prepared by pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from the common of the com SOURCE INFORMATION:

one male donor.

The clone may be obtained either from Genome Systems, (http://www.resgen.com) or Research Genetics, 1 (http://www.resgen.com); or from Pieter de Jong.

VECTOR: pCYPAC2
NEIGHBORING SEQUENCE INFORMATION:
ACTUAL start of this clone is at base
actual end is at 126462 of RP4-747G18. position 1 of RP4-747G18;

jor. correct. double stranding from 7 be guaranteed although submitted assembly organism="Homo sapiens" ocation/Qualifiers, .126462 nteed although their sequence fidelit Digests using EcorV and HindIII are from 79862 to 80357 in the PAC RP4-747G18 can though their sequence fidelity is believed to

FEATURES repeat_region repeat_region repeat_region /rpt_family="Alu" 578. ..898 /rpt_family="Alu" 1238. .1373 clone clone="RP4-747G18" map="7g22-31.1" chromosome="7" db_xref="taxon:9606" lib="RPCI-4"

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Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E., Robinson,D., Jones,M., Buckingham,J., Chasteen,L., Thompson,S., Goodwin,L., Bryant,J., Tesmer,J., Mincke,L., Longmire,J., White,S., Tatum,O., Campbell,C., Fawcett,J., Maltbie,M., Bussod,M., Sutherland,R., McMurry,K., Han,C. and Deaven,L.
Submitted (20-MAY-1999) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, NM 87545, USA
                                                                                                                                                                                                                                                                                                                            ACUU7616 132492 bp DNA linear PRI 18-DEC-2003
Homo sapiens chromosome 16 clone RPI1-547D14, complete sequence.
AC007616
                                                                                                                                                                           DOE Joint Genome Institute, Stanford Alamos National Laboratory.
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                            Direct Submission
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Pred. No. 4.5e-42;
1; Mismatches 72;
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Abraham, H.,

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Collins, S.,

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                                                                                                                                                                                                                                                                                                                                                SEQUENCE,
AC027249
                                                                                                                                                                                                                                                                                                                                                                         AC027249 145679 bp DNA linear Homo sapiens chromosome 11 clone RP11-753E7 map 11, SEQUENCE, 35 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (18-DEC-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 18, 2003 this sequence version replaced gi:21700556.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is not the entire sequence of the clone (entire sequence 168.9kb). It is clipped at the overlap with AC007613. The number of bases overlapped is 29296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www.shgc.stanford.edu
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                                                                                                         Hominidae; Homo.
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                          AC027249.2 GI:7651924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: Phrap Quality >=40 100% of Estimated Total Number of Errors is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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(bases 1 to 145679)
irren,B., Linton,L., Nusbaum,C. and Lander,E.
omo sapiens chromosome 11, clone RP11-753E7
                                                                                                                                 ammalia; Eutheria; Euarchontoglires; Primates;
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                                                                                                                                                                                                                                    HTGS_PHASE1; HTGS_DRAFT sapiens (human)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 155.4;
Pred. No. 4.6
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                                                                                                                                        Catarrhini;
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WORKING DRAFT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 27, 2000 this sequence version replaced gi:7331619. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 129416 bases at least Q40
Consensus quality: 137400 bases at least Q30
Consensus quality: 140385 bases at least Q20
Insert size: 154000; agarose-fp
Insert size: 142279; sum-of-contigs
Quality coverage: 3.9 in Q20 bases; agarose-fp
Quality coverage: 4.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 35 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                      note="assembly_fragment"
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/clone_lib="RPCI-11 Human Male BAC"
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sequence.
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Homo sapiens
                                                                                                                                                                                 CTTGAACCCAGGAGGCGGAGGCTGCAGTGAGCCAAGATTCCGTC 8285
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/estimated length=100

3965. 5223

/note="assembly_fragment"

5224. 5323
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21734. .24035
/note="assembly_fragment"
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24136. .26117
/note="assembly_fragment"
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5324. .7019
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9278. .11580
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120. .9177
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  GI:32400666
                                        183444 bp DNA linear PRI 02-JUL-2003 genomic DNA, chromosome 11 clone:RP11-832N8, complete
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Pred. No. 4.8e-42;
1; Mismatches 62
                                                                                                                                                       346
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                                                                                                                                                                                           202138 bp DNA linear
Homo sapiens chromosome 11 clone RP11-531E6 map 11,
SEQUENCE, 22 unordered pieces.
AC018423
              1 (bases 1 to 202138)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-531E6
                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                           Homo sapiens
                                                                                                                                                         AC018423.4 GI:10045404
HTG; HTGS_PHASE1; HTGS_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
On Jul 1, 2003 this sequence version replaced gi:31790714.
Location/Qualifiers
                                                                   Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pub1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-JAN-2000) Masahira Hattori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hattori, M., Ishii, K., Toyoda, A., Fujiyama, A., Yada, T., Totoki, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hattori, M., Ishii, K., Fujiyama, A., Yada, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                            CTTGAACCCAGGAGGCGGAGGCTGCAGTGAGCCAAGATCGCGACAGAGCAAGATTCCGTC 173947
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAG-CAGAGTGAGACKCCGTC
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blished Only in Database (2000)
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                                                                                                                                            sapiens (human)
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/db_xref="taxon:9606"
/chromosome="11" ·
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/mol_type="genomic DNA"
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                                                                                                                                                     HTGS_DRAFT
                                                                                                      Chordata;
                                                                                    Euarchontoglires;
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Totoki, Y.,
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Pred. No. 5.4
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                                                                                                      Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taylor, T.D., Watanabe, H.
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5.4e-42;
hes 62;
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                                                                                      Primates;
                                                                                                    Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Institute of Physical
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                                                                                      Catarrhini
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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pierre, N., Pollara, V., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiilev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-DEC-1999) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 021141, USA On Sep 9, 2000 this sequence version replaced gi:6649385. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L3744

Center clone name: 531 E 6

Center clone name: 531 E 6

Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 188769 bases at least Q40
Consensus quality: 195790 bases at least Q30
Consensus quality: 195790 bases at least Q20
Insert size: 210000; agarose-fp
Insert size: 210000; agarose-fp
Quality coverage: 4.4 in Q20 bases; sgarose-fp
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it
be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
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gap of 100 bp
contig of 3676 bp in length
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gap of 100 bp
contig of 2026 bp in length
gap of 100 bp
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                                                                                          g of 6053
f 100 bp
g of 6489
  100 bp
g of 4036 bp :
100 bp
of 5595 bp :
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of 5817 bp
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of 38927 bp
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sum-of-contigs
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FEATURES
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173877
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199612
199712
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106558
106658
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144591
155575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_end:SP6
vector_side:left"
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76350. .76449
/estimated_length=100
76450. .82044
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72214. .72313
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3555. .53654
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4528. .14627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="RP11-531E6"
clone_lib="RPCI-11 Human
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90416: gap of 100 bp
96732: contig of 6316 bp in length
96832: gap of 100 bp
106557: contig of 9725 bp in length
106557: contig of 9725 bp in length
114415: contig of 7758 bp in length
114515: gap of 100 bp
122744: gap of 100 bp
132174: contig of 829 bp in length
132274: gap of 100 bp
132174: contig of 9330 bp in length
132274: gap of 100 bp
14490: contig of 12216 bp in length
144590: gap of 100 bp
155574: gap of 100 bp
155574: gap of 100 bp
155574: gap of 100 bp
173876: contig of 18202 bp in length
173976: gap of 100 bp
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RESULT 44
AC099489
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

AC099489 204493 bp DNA linear PRI 04-FEB-Homo sapiens chromosome 16 clone CTD-3088G3, complete sequence. AC099489

PRI 04-FEB-2003

SOURCE

AC099489.2 GI:28201477 HTG. Homo sapiens (human)

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Matches 203; Conserv
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102122
                                                                                                               102242
                                                                                                                                                                      102302
                                                                                                                                                                                        141 TCGAGACCATCCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAAATACAAAAAAATAGC 200
                            320
                                                                                                                                          201
                                                                           TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAG-CAGAGTGAGACKCCGTC 319
                                                                                                               TGGGTGTGGTGGCCCACGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGACAGGAGAGAATCG 102183
                                                                                                                                                                    TCGAGATCAGTCTAGCCAACATGGTGAAAACCTTGTCTCTACTAAAAAATACAAAGATTAGC 102243
TCAAAAAAAAAAAAAAAAAAGGAGAA 102096
                                                                                                                               TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGC 260
                         ТСААВАССААСААСААВААССАВАВА 346
                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                       /estimated_length=100
144591. 155574
/note="assembly_fragment"
15575. 155674
/estimated_length=100
155675. 173876
/note="assembly_fragment"
173877. 173976
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/note-"
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82145. .90316
note="assembly_fragment"
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82045. .82144
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22845. .132174
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.6. .122744
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                                                                                                                                                                                                                                                                                  Score 155.4; DB 12;
Pred. No. 5.6e-42;
1; Mismatches 62;
                                                                                                                                                                                                                                                                                                             DB 12; Length 202138;
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                                                                                                                                                                                                                                                                                     1; Gaps
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RESULT 45
AL355388
LOCUS
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    DEFINITION
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                    14539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198;
                                                                                                                                                                                                                                                                                                                                         203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 GCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATC 142
  AL355388
Human DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.4.
NOTE: Shatter libraries failed to verify the dinucleotide repeat
region 65514-65789. Unsure number of repeat copies 65514-65789.
Forced join at 65675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (04-FEB-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 4, 2003 this sequence version replaced gi:16930905. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (15-NOV-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US 3 (bases 1 to 204493)

DOE Joint Genome Institute, Stanford Human Genome Center and Los
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alamos National Laboratory.
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DOB Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct
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DOE Joint Genome Institute,
Alamos National Laboratory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                     GAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTG
                                                                                                                                                                                                            TGAACCCAGGAGGAGGAGAATTGCTTGAACCCTGGGCGACAGAGCGAGACTCCATCTCA
                                                                                                                                                                                                                                                                                                                                      GGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTG
                                                                                                                                                                                                                                                                                                                                                                                GAGACCAGCCTGGCCAACACGGTGAAACCCCCAACTCTCCTAATAATAAAAAAATTAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCTGTAATCCCAGCACTTGGGGAGGCCAAGGCGGGTGGATCACTTGAGGTCAGGAGTTT
                                                                                                                                                                   ААААСААСААСАААААААССАТАА 353
                                                                                                                                                                                                                                                      AGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCA 322
                                                                                                                                                                                                                                                                                             GGCCTGGTGGCATGCGCAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATTGCT 14658
                                                                                                                              AAAACAAAACAAAACCAAAAACTAAA 14749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
    DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="NOTE: Shatter libraries failed to verify the dinucleotide repeat region 65514-65789. Unsure number topies 65514-65789. Forced join at 65675."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="CTD-3088G3"
65514. .65789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205463 bp DNA linear PRI 18-MAY-2005 sequence from clone RP11-336K24 on chromosome 1 Contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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73.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 155.4; DB 5
Pred. No. 5.7e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72;
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94598, USA
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                gene
                                                                                                                                                                                           mRNA
                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
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join(complement(4923..5084),complement(complement(4130..4186),complement(41130.28.24:141244..141317),complement(AL139128.24:140824..141015),

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complement complement

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gene="RIT1

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clone="RP11-336K24"

organism="Homo sapiens" /mol_type="genomic DNA" Location/Qualifiers

. .205463

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Clone requests: clonerequest@panger.ac.uk
On Mar 29, 2003 this sequence version replaced gi:28446036.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1
RP11-336K24 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the 5' end of the RIT1 gene for Ras-like without CAAX 1, the gene for a novel protein (KIAA0907), the ARHGEF2 gene for rho/rac guanine nucleotide exchange factor (GEF) 2, four novel genes, the SSR2 gene for signal sequence receptor beta (translocon-associated protein beta), the Clorf6 gene for chromosome 1 open reading frame 6, the gene for mitogen-activated protein-binding protein-interacting protein (MAPBETP), the RAB25 gene for RAB25 (member RAS oncogene family), the 5' end of the LMNA gene for lamin
Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cambridgeshire, CB10 1SA, UK. B-mail enquiries: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Cnoroata; Cianaca; Tercoscoro, Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL355388.30 GI:29367464
HTG; ARHGEF2; Clorf6; KIAA0907; LMNA; MAPBPIP; RAB25; RIT1; SSR2.
                                                                                         Center code: SC
                                                                                                                             Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                     http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo.
1 (bases 1 to 205463)
                                                                                                                                                                                                                 VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \mathtt{A/C} and three CpG islands, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                         Genome Center
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gene
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           SdC
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complement (AL139128.24:141244. .141317),
complement (AL139128.24:141116. .141123),
complement (AL139128.24:140824. .141015),
complement (AL139128.24:136911. .137131))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(complement (4558..4565), complement (complement (4130..4186), complement (AL139128.24:141244..141317), complement (AL139128.24:140824..141015), complement (AL139128.24:136901..137131))
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complement (AL139128.24:141244 . .141317),
complement (AL139128.24:140824 . .141015),
complement (AL139128.24:136787 . .137131))
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complement (AL139128.24:141244. .141317),
complement (AL139128.24:1410824. .141015),
complement (AL139128.24:134321. .137131))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="RIT1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard_name="OTTHUMP00000015933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            locus_tag="RP11-10106.4-002"
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lement (AL139128.24:140824.
lement (AL139128.24:136911.
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. .141015),
. .137131))
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Similarity
                                                                                                                             TGGGCATGGTGGCACACCCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                 TCGAGACCAGCCTGACCAACAAGGTGAAACCTCGTCTCTACTAAAAATACAAAAATTAGC
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                                                                                                                                                                                                                                                                                                    ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
TECTTEAACCCGGGAGGCGGAAGTTGCAGTGAGTCTAGATCGCAGAGTGAGACTCCGTCC 177456
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                                                                                                   CGAGCATGGTGGCAGACGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGACAG--GAGAAT 177396
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Ĭocus tag="RP11-336K24.1-001"
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FETSAAYRYIDDVFHALVREIRRKEKEAVLAMEKKSKPKNSVWKRLKSPFRKKKDSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="RP11-336K24.1"
/locus_tag="RP11-336K24.1-003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="RP11-336K24.1"
/locus_tag="RP11-336K;
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/db_xref="InterPro:IPR005225"
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                                                                                                                                                                                                                                                                                                                                                                                                                          38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                     Score 155.4; DB 5;
Pred. No. 5.7e-42;
L; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Em: AB020714.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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.17367,19312.
.23055,23392.
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.20836,22976. .23055.
.28077))
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Homo sapiens chromosome 16 clone CTD-2169M19,
ACO26423
ACO26423,9 GI:29020775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (18-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 18, 2003 this sequence version replaced gi:18057078.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (04-JAN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US 4 (bases 1 to 116130)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (22-MAR-2000) Production Sequencing Facility,
Genometric (2800 Mitchell Drive, Walnut Creek, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: Phrap Quality >=40 100% of Sequence; Estimated Total Number of Errors is 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Finishing Completed at Stanford Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     www.jgi.doe.gov
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DOE Joint Genome Institute.
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Alamos National Laboratory.
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                                                                                                                                                                                                                                                                                                              h 38.8%;
Similarity 74.5%;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dominidae; Homo
TGAGATCGCAGAGTGAGCCGAAATCACAGAT-----CACAGAGTGAGCAGAGTGAGAC
                                                                                                                                                                                                                                                         ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                            CGGGCTTGGTGGCATGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGGAAGGT 11486
                                                                                     TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                        TCGAGACCAGCCTGGCCAACATGGTGAGACCTCATCTCTACTAAAAAATACAAAAATTAGC
                                                                                                                                                                            TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                   CAAAAACAACAACAAAAAAAAAAAAAAAACCATAAGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                                                 clone="CTD-2169M19"
                                                                                                                                                                                                                                                                                              Score 155.2; DB 5
Pred. No. 5.1e-42;
1; Mismatches 64
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18 Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Alsbrooks, S.L., Amaratunge, K., Blankenburg, K., Bonnin, D., Alsbrooks, S.L., Amaratunge, K., Blankenburg, K., Bonnin, D., Burbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Bydn, N.C., P., Buhay, C., Burch, P., Burkett, C., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Brown, E., Chacko, J., Chavez, D., Carron, T.F., Carter, M., Cavazos, S.R., Chack, N.J., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Ding, Y., Dinh, H., Dederich, D.A., Daulaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Eascotto, M., Falla, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Guevara, W., Gunarathe, P., Hale, S., Harris, K., Harris, M., Havlak, P., Mandle, D., Manda, R., C., Harris, K., Harris, M., Havlak, P., Manda, C., C., Harris, K., Harris, C., Harris, K., Harris, M., Havlak, P., Manda, C., C., Larris, K., Harris, M., Harris, C., Larris, K., Harris, M., Harris, C., Larris, K., Harris, M., Havlak, P., Manda, C., C., Larris, K., Harris, C., Larris, K., Harris, M., Harris, C., Larris, K., Harris, M., Harris, C., Larris, K., Larris, M., Larris, C., Larris, M., La
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                                                                                                                                     Worley,K.C.
Direct Submission
Submitted (02-SEP-2000) Human Genome Sequencing Center, Deparence of Medicine,
                                                             Baylor Plaza, Houston, 3 (bases 1 to 177640)
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Homo sapiens 12 BAC RP11-206B11 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
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Mammalia; Eutheria;
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                                                                                                                                                                      SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the
                                                                                                                                                                                                                                                                                                                                                                              unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (spect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANNOTATION OF FEATURES: STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and
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On Oct 22, 2002 this sequence version replaced gi:15809129.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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Baylor Plaza, Houston,
7 (bases 1 to 177640)
Worley,K.C.
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Baylor Plaza, Houston,
(bases 1 to 177640)
QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error ratio less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
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Repeats are identified using RepeatMasker (A. Smit and P. Green,
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FEATURES

Location/Qualifiers

http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreita, P., FitzHugh, W., Gage, D., Galgan, J., Gardyna, S., Glode, S., Goyette, M., Graham, L., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Tones, C., Kann, L., Karatas, A., Tones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 178079)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 1, clone RP11-206C14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC068929 178079 bp DNA linear Homo sapiens chromosome 1 clone RP11-206C14 map 1, SEQUENCE, 11 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC068929.3 GI:11597096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGCTCTGGTGACTCACACCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGG 97453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAAAACAAAACAAAACAAAACAAAA 97367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   СААЛААСААСЛАЛАЛАСААЛАЛА 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 178079)
Center project name: L7679
Center clone name: 206 C 14
----- Summary Statistics
Sequencing vector: M13; M77815; 42% of reads
Sequencing vector: Plasmid; n/a; 58% of reads
                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                            Center code: WIBR
Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WORKING DRAFT
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                                                                                misc_feature
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8649
9686
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8649. .9685
                                                                                        /estimated
22787. .34
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                                                                                                                                                                                                     14638. .22686
                                  /note="assembly_fragment"
34298. .34397
                                                                                                                                            22687. .22786
                                                                                                                                                                note="assembly_fragment"
                                                                                                                                                                                                                                                     /note="assembly_fragment"
14538. .14637
                                                                                                                                                                                                                                                                                  ll308. .14537
                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment"
l1208. .11307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'mol_type="genomic DN
'db_xref="taxon:9606"
                                                                                                                                                                                                                   estimated_length=100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="RP11-206C14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            length=100
                                                                                                            length=100
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Insert size: 170000; agarose-fp
Insert size: 177079; sum-of-conetigs
Quality coverage: 6.2 in Q20 bases; agarose-fp
Quality coverage: 5.9 in Q20 b.
NOTE: This is a 'working draft' sequence. It currently
consists of 11 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 172732 bases at least Q40
Consensus quality: 175502 bases at least Q30
Consensus quality: 176567 bases at least Q20
ocation/Qualifiers
                                     gap of
                                                                                                                 gap of
                                                                                                                                                                                                   contig
gap of
                                                                                                                                                                                                                                                                                   contig
gap of
                                                                                                                                                                                                                                                                                                                       contig of 1037 bp in length
gap of 100 bp
contig of 1422 bp in length
gap of 100 bp
                                                                                                                                                           contig
                                                                                                                                                                                                                                                                                                                                                                                                         contig
                     contig of 26154 bp in length
                                                                                                                                                                                                                                           gap of
                                                                                                                                                                                                                                                                                   of 3230
                                                                                                                     of 13453 bp in length
100 bp
of 19330 bp in length
100 bp
                                                                                                                                                                                                                    of 8049 bp in length
100 bp
of 11511 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                           of 8548 bp in length
100 bp
                                          100 bp
                                                          of 63373 bp
                                                                                                of 20972 bp
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REFERENCE
AUTHORS
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ORGANISM
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DEFINITION
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AL162384
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                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                              VERSION
                                                                                                                                                                     TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81
                                                       Direct Submission
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
On Mar 12, 2001 this sequence version replaced gi:12831806.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 ALI62384 68465 bp DNA linear PRI 18-MAY-200 Human DNA sequence from clone RPI1-21817 on chromosome 9 Contains novel gene similar to RAN binding protein 6 (RANBP6), the 5' end can novel gene, a novel gene and a CpG island, complete sequence.
                                                                                                                                                                                                             Tracey,A.
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                       AL162384.14 GI:13274331
HTG; CpG island; RANBP6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGCTCTGGTGACTCACACCTGTAGTCCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGG 130370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAAAACAAAACAAAACAAAACAAAA 130284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGAAAGGTGGATCACCTGAGGTCAGGAGT 130490
                                                                                                                                                                                                                            (bases 1 to 68465)
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151826. .151925
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38453. .151825
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57381. .88352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment"
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17951..67280
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8079
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Pred. No. 6.2e-42;
1; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12;
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FEATURES
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RP11-21817 is from the library RPCI-11.1 constructed by the group of the Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     //www.chori.org/bacpac/home.htm
                                                                                                                                                                      /locus_tag="RP11-21817.1-001" complement(7378. .7383) /locus_tag="RP11-21817.1-001"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Clone_left_end: RP11-21817"
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Q96E78 Q9EQ30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (AL353606.12:14362. .14562)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (AL365360.9:149198.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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                                       AAH19309 000410 060518
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LAVKLETHASMRKKLCDIFAVLARNILIDEDGTNHWPEGLKFLIDSIYSKNVVLMEVAL HVFWHFPGIFGTQERHDLDIIKRLLDQCIQDQEHPAIRTLSARAAAAFVLANENNIAL FKDFADLLPGILQAVNDSCYQDDDSVLESLVEIADTVPKYLGPYLEDTLQLSLKLCGD

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RESULT 50
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                        CTTGAACCCGGGAGGTAGAGACTGCAGTGAGCCGAGACTGCGCCACTGCATGACAGAGCG 24050
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAG------CAGAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGGCATGGTGGCACACCCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAAGACCAGCCTGACCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                          AGACKCCGTCTCAAAAACAACAACAAAAAAAACAAAA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGGTGTGGCACACGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGATGGAGAATCT 23990
                                                                                                                                                                                                            AGACACCATCTCAAAAAAAAAAAAAAAAAAAAAGGAA 24085
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/db_xr
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complement (join(<9894. .10679,11795. .11809))

/locus_tag="RP11-21817.1-002"

/standard_name="OTTHUMP00000021040"
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NHPVVIGPNNSNLPKIISIIAEGKINETINYEDPCAKRLANVVRQVQTSEDLWLECVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARIRGPEYLAQMWQPICDPLIKAIGTEPDTDVLSEIMNSFAKSIEVMGDGCLNDEHLELGAIRGPEYLAQMWQPICDPLIKAIGTEPDTDVLSEIMNSGACOVYILTKYSDILHS
EELGGILKAKLEGHPKNQELFQVKRQEENPDQVGMSLOIEDDIIEHCSPTSFKYVSDILHS
LFSTYKEKILEWFEQLLFLIVHLICSSREWPDRQWGLCIFDDIIEHCSPTSFKYVSF
RWPMLLNMRDNNPEVRQAAAYGLGVMAQPGGDDYRSLCSEAVPLLVKVIKCANSKTKK
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KDFQQYLPLVIEPLIKTASAKPDVALLDTQDVENMSDDDGWQFVNLGDQQSFGIKTSG
LEAKKTACQMLVYYAKELREGFVEYTEQVVKLMVPLLKFYFHDNVRVAAAESMPFLLE
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IGEGCHQQMESILDETVNSVLLFLQDPHBFVRAAASTTTIGQMATUPFAPNFQKKFHETV
IAALLRTMENGGNQRVGSHAASALIFFIEDCPKSLLVLYVDSNYKNLHSVLVLVIKLGEI
IRNGTKLALEQIVTTIASVADTIEEKFVPYYDIFMPSLKHIVELAVQKELKLLRGKTI
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Carron, T.P., Carter, M., Cavasos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Chawlay, I., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Chawlay, I., Chavez, D., Claveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Davis, C., Davy-Carroll, L., Ding, Y., Dinh, H.H., Dauthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foseer, P., Esanhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foseer, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunarathe, P., Hale, S., M., Hamilton, K., Han, J., Hernandez, O., Hodgson, A., Hogues, M., Halloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hant, M., Hogues, M., Hamilton, K., Han, J., Jackson, E., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Jockson, E., Jackson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, M., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Li, Chtarge, O., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lux, Y., Lucier, A., Luna, R., Mazi, M., Martinez, E., Massey, E., Mariney, E., McLeris, R., Miner, G., Miner, Z., Mitchall, T., Metzoher, S., Mohabat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Sonakke, T., Sparke, A., Stanley, H., Stone, H., Shim, C., Shooshtari, N., Sisson, I., Sodergren, E., Sonake, T., Sparke, A., Stanley, H., Stone, H., Mang, O., Warsen, R., Washington, C., Wallington, S., Worley, K., Wang, O., Warsen, R., Washington, C., Wallington, S., Worley, K., Wang, O., Wallington, S., Worley, K., Wang, O., Wallington,
Submitted (01-JAN-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                            Submitted (21-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
[bases 1 to 73433]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (11-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 73433)
Worley, K.C.
Direct Submission
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Albrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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COMMENT

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Genes and Region of sequence similarity are identified by BI (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to t EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Jan 1, 2003 this sequence version replaced gi:23264934. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are o sequenced and submitted once, so the requence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
                                                                                                                                                                                                                                                                                                                         complement (1166.
                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="(TA)n"
915._.1149
                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="L1MC5"
842. .888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                       complement (2163.
                                                            ,zgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function="clone overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'mol_type="genomic DN
'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="overlaps bases 170628. .172558 of clone AC023509"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="RP11-774122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                     _family="AluSp/q"
                      _family="AluSg"
                                                                                                   _family="AluJo"
                                                                                                                                                                                                                        _family="L1MC5"
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                                                                                                                                                                                family="AluJo"
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                                                                                                                                           _family="AluSp"
                                                            family="L1MC5"
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                                         .2467)
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                                                                                                                                                                                                                                                                        ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                           TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAAATACAAAAAATAGC
        CGAGATC----ATGCCACTGCACTCCAGCCTGGGCGAAGAGCAGGACTCCATCT
                                               TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                       TGGGCACGGTGGCAGGCGCCTGTAATCCCAGCTACTCAGGAGGCACAGGTTGCAGTGAGC
                                                                                                                            TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                    TCAAGACCAGCCAAGATGGTGAAACCCTATCTCTACTAAAAATACAAAAATTATC
                                                                                                                                                                                                                                                   ACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGGGAGGATCATCTGAGGTCAGGGGT
                                                                                                                                                                                                                                                                                                                              Conservative
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/rpt_family="AluSp"
4904. .5211
                                                                                                                                                                                                                                                                                                                                                                                                /function="low quality"
11840. .12010
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9675
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2847. .2962
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2538. .2846
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0267. .10546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family="AluSg"
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                                                                                                                                                                                                                                                                                                                                Score 155; DB 5; 1
Pred. No. 4.8e-42;
1; Mismatches 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality."
                                                                                                                                                                                                                                                                                                                                                                     Length 73433;
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FEATURES

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Adm20017 Human rep
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Abl9805 Human rep
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Aef92655 Human Rass
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Ab4883568 Human DAA
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Adg41559 Human res
Adi97333 Human res
Adi19731 Osteoarth
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immune/haematopoietic antigen genomic sequence

SEQ ID NO:38713.

2000US-0179065P 2000US-0180628P 2001WO-US001354

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Query Match
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Matches 201;
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17-NOV-2000; 2000US-0249264P.
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08-DEC-2000; 2000US-0251989P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of a number of ovarian and breast antigens. These are shown in AAI62467-AAI62572 and AAW42240-AAW42345. The sequences can be used in the diagnosis, prevention and treatment of breast and ovarian cancers, and their metastases. The present sequence is a genomic sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 270; 520pp + Sequence Listing; English
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73.9%;
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AC AAK87161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) creatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disporders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to complement the patients own production of (I). Additionally, (I) concept and the abost cell and culturing the cell to express the complement caids into a host cell and culturing the cell to express the complete acids into a host cell and culturing the cell to express the complete and treat immune/haematopoietic-related diseases, especially concers and cancer metastases of haematopoietic antigen genomic concers from the present invention. AAK54942 to AAK87694 represent buman immune/haematopoietic antigen genomic represent sequences used in the exemplification of the present invention.
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08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-025199P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasi
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer:
                                Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41973.
                                                                      07-NOV-2001
                                                                                                      AAK87161;
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                                                                                                                                      standard; DNA;
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                                                                    (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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 WO200155320-A2
                            Homo sapiens.
                                                     cancer; gene therapy;
                                                                     Human; reproductive system related antigen; reproductive system disorder;
                                                                                                 Human reproductive system related antigen DNA SEQ ID NO: 6505.
                                                                                                                             21-NOV-2001
                                                                                                                                                          AAL03817;
                                                                                                                                                                                    AAL03817 standard; DNA; 16163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 represent sequences used in the exemplification of the present invention
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02-MAR-2000;
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Rosen CA,
                                            (HUMA-) HUMAN GENOME SCI INC
  Barash
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2000US-0246527

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2000US-0246524P.
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SC,
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RESULT 6
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ID ADA02
XX ADA0
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SXCCCCCCXXXX
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening; gene; ds.
                                                                                                               WPI; 2003-587068/55.
                                                                                                                                                                                                                                                                                  26-DEC-2001; 2001US-00035832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
                                                                                                                                                                         Morris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human IRF2 carcinoma associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA02750;
                                                                                                                                                                                                                                                                                                                                               26-DEC-2002; 2002WO-US041414.
                                                                                                                                                                                                                                                                                                                                                                                                        17-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA02750 standard; DNA; 96593 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16163 BP; 5062 A; 3448 C; 3239 G; 4414 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   İsolated nucleic acid molecule encoding a reproductive system antigen used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                  (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-465570/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8232 GGAGTTTGAGATCAGTCTGGCCAACATGGTGAAACCCCCGTCTCTACTAAATATACAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8172 GGTTCACGCCTGTAATCCCCAGCACTCTGGGAGGCCGAGGCCGGGTGGATCACCTGATGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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73.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene, SEQ ID NO:1268
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New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.

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유정
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cci acid sequences from mouse and human (ADA)1482-ADA)3094) and to combinant carcinoma associated proteins (CAP) encoded by them. The cci invention also encompasses expression vectors and host cells comprising a CC invention also encompasses expression vectors and host cells comprising a CC A nucleic acid, a polypeptide (especially an antibody) that specifically cc. binds to the protein, and a biochip comprising CA nucleic acid or cci fragments thereof. The sequences of the invention were identified using CC oncogenic retroviruses, which insert into the genome of the host organism CC at random. Many of these do not carry transduced host oncogenes or cc pathogenic retroviruses, which insert into the genome of the host organism CC pathogenic trans-acting viral genes, meaning that cancer incidence is a CC direct consequence of the effects of proviral integration into host cc protooncogenes. The CA nucleic acid sequences can be used to diagnose CC carcinoma (especially breast cancer, prostate cancer, lymphoma or CC leukaemia) or a propensity to carcinoma by determination of the sequence cc carcinoma content and in screening and evaluating drug candidates. The content sequence represents a specifically claimed human CA nucleic acid content and in screening and evaluating by the carcinome candidates. The present sequence of the invention. Note: The complete sequence data for this sequence of the invention. Note: The complete sequence data for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                      04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                 26-DEC-2001; 2001WO-US051291
                                                           30-JAN-2003.
                                                                                             WO2003008583-A2
                                                                                                                                   Homo sapiens
                                                                                                                                                                     human; ds; cytostatic; cancer; neoplasm; adeno
                                                                                                                                                                                                                                  Human IRF2
                                                                                                                                                                                                                                                                                                            ADB72488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Sines 216;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141
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                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP;
                                                                                                                                                                         atic; gene therapy; vaccine; carcinoma;
adenocarcinoma; sarcoma; gene.
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                                                                                                                                                                                                                                                                        entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 158.4; DB 9;
Pred. No. 1.8e-33;
1; Mismatches 57;
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02-DEC-2002; 2002WO-US038582

05-JUN-2003. WO2003045230-A2 Homo sapiens Cytostatic;

c; gene therapy; vaccine; cancer; carcinoma-associated transmembrane; intracellular; ds.

gene;

Ç,

01-JAN-2004

(first entry)

Irf2

genomic sequence

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RRESULT 8
ADC85230
ID ADC86
XX
AC ADC86
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PT 01-J
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CYCC
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COS Homc
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Best Local Similarity
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23-OCT-2001; 2001US-00004113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-00997722.
20-DEC-2001; 2001US-00034650.
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Pred. No. 1.8e-33;
1; Mismatches 57
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Matches 216;
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                                                                                                                                                                                                         Human carcinoma associated (CA) nucleic acid
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22-DEC-2000; 2000US-00747377
02-MAR-2001; 2001US-00798586
                                        30-NOV-2001; 2001US-00997722.
                                                                                               US2004072154-A1.
                                                                                                                                                  cytostatic.
                                                                                                                                                                 carcinoma associated protein;
                                                                                                                                                                           Human; carcinoma associated nucleic acid; CA nucleic acid; gene; ds;
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                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                      01-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant nucleic acid comprising a nucleotide sequence of a the carcinoma-associated (CA) genes, useful for screening for drug candidates for diagnosing or treating carcinomas.
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Pred. No. 1.8
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                                                                                                                                                              carcinoma; leukaemia; lymphoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC also relates to a host cell comprising a recombinant nucleic acid or CC expression vector, an expression vector comprising a recombinant protein, a method of screening for drug candidates, a CC method of screening for a bioactive agent capable of binding to a CC method of screening for a bioactive agent capable of modulating the carcinoma associated protein (CAP) encoded by a nucleotide sequence, a CC method of screening for a bioactive agent capable of modulating the CC carcinoma drug, a method of evaluating the effect of a candidate carcinoma drug, a method of diagnosing carcinoma, a method of treating carcinomas, a method of meutralising the effect of a CAP and a method of diagnosing carcinoma or CC propensity to carcinoma. A method of evaluating the effect of a candidate CC carcinoma drug comprises administering the drug to a patient, removing a CC cell sample from the patient and determining alterations in the cell capable of diagnosing carcinoma comprises determining the expression of activation of a gene comprises determining the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cc method of diagnosing carcinoma comprises determining the expression of come or more genes comprisions the mucleic acid sequence in a first tissue type of a first individual and comparing the expression of the gene from cc a second normal tissue type from the first individual or a second cunaffected individual, where a difference in the expression indicates that the first individual has carcinoma. A method of inhibiting the activity of a CAP comprises binding an inhibitor to the CAP. Treating c carcinomas comprises administering to a patient an inhibitor of CAP. Neutralising the effect of a CAP comprises contacting an agent specific for the CAP. The polypeptide specifically binds to the protein encoded by the nucleic acid. It comprises an antibody that specifically binds to the protein encoded by the nucleic acid. The nucleic acids are useful for preparing a composition for diagnosing or treating carcinoma e.g., associated (CA) nucleic acid of the invention. Note: The sequence data for this patent did not form part of the printed specification but was cobained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seqdata.uspto.gov/sequence.html.
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  CTTGAACCCAGGCGGCGGAGGTTGCAGTGAGCCGAGATCGCACCAGCTTGGGTGACAAGC 18456
                                                                                          TGAGATCGCAG------AGTGAGCCGAAATCACAGATCACAGAGTGAGCAGA 306
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Gaps

RESULT 10 ACN44354/c

ACN44354;

18-NOV-2004

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The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of bindating to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for neutralizing the effect of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CAP genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586AI, for which no sequence data was published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 31898 BP; 7315 A; 9118 C; 8770 G; 6695 T; 0 U; 0 Other;
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   321 CAAAAACAACAACAAAAAAAAAAAAAACCATAAGACATTGTCCATCTGCGGTTCCCAGA 379
                                                                                                                                                                                                                                         ACGCCTATAATCCCAGCACTTTGGAAGGCCAAGGTGGGCGGATCACTTGAGGCCAGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 760; Opp; English.
                                                                                                                          TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                    CGAGACCACGCCTTTGCACTCCAGCCTGGGCGA-----CAGAGCGAGACTCTGTCT
                                                                                                       CCGGAGTGGTGGTGGCCCTGTAGTCCCAACTACTCGGGAGGCGGAGGTTGCAGTGAGC
                                                                                                                                                                        TCGAGACCAGCCTGGCCAAAATGGTGAAACCCCCGTCTACTAAAAAATACAAAAATTAGC
                                                                                                                                                                                        TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                              ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
                                                                 Conservative
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72.6%;
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Pred. No. 8.8e-33;
                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                          Length 31898;
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single nucleotide polymorphism.
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   /standard_name= "Single nucleotide polymorphism"
/note= "Variable nucleotide A,G"
12746
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/note= "Variable nucleotide T,C"
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note= "Variable nucleotide G,T"
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WPI; 2003-328604/31

Morris

WO2003073826-A2

Homo sapiens

12-SEP-2003

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Query Match
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single nucleotide polymorphisms associated with examination and assessment of susceptibility to
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(KAMO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34796 BP; 7631 A; 9152 C; 9368 G; 8645 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence represents a polymorphic gene of
AAAAACAAAACAAACAAACAAACAAAAAAAAACAAC
                                                                                                                                                                         TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                                                 TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
                                  САДАДАСДАСДАДАДАДАДАДАДАДАДССАТДАДАС 356
                                                                                                   TGAGATCGCAGAGTGAGCCGAAATCACAGAGTCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                                                                                                                                                                              ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                       TTGAGACCAGCCTGGCCAACATGATGAAACCCCCGCCTCTATTAAAAATACAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 150; Opp; Japanese.
                                                                                                                                                 TGGGCATGGTGGCGAGTGCCTGTAGTCCCAGCTACTCAGGAGGCGGAGGTTGCAGTGAGT
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/note= "Variable nucleotide G,T"
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Pred. No. 1.7e-32;
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Human; breast specific gene; breast cancer; differential expression; cytostatic; gene therapy; gene; ss.

Human breast cancer associated coding sequence SEQ ID NO:

04-DEC-2002 ABT10719

(first entry)

ABT10719 standard; cDNA; 122748

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer. The methods are useful in diagnosing, treating, detecting the progression, and in monitoring treatment of breast cancer in patients. The methods are also useful as a screening tool for agents that modulate the onset or progression of breast cancer. The breast cancer genes may be used as diagnostic markers for the prediction or identification of the malignant state of breast tissue, for confirming the type and progression of cancer, and for drug screening and ssays. The present sequence is a coding sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diagnosing breast cancer in a patient comprises detecting the 1-
gene expression in cell or tissue samples, where a differential
expression is indicative of breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Orr MS,
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AAC79009;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nation M,
                                                                                                                                                                                                                                                                   TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                                                                TTGAGACCAACCTGACCAACATGGTGAAAACCCCCACCTCTACTAAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                    TCGAGACCATCCTGGCCAACATGGTGAAAACCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                  ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122748 BP;
                                                                                                               CAAAAAAAAGAAAGAAAGAAAAGAAAAGAAAAGAAAA 114043
                                                                                                                                            САЛАЛАСАЛСАЛАЛАЛАЛАЛАЛАЛАЛАССАТАЛСАСА
                                                                                                                                                                               TGAGATTGTGCCGTTGCACTCCAGCCTGGGCGA----
                                                                                                                                                                                                             TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                                                                                                TGGGCATGATGGCAGTTGCCTGTAATCCCAGCTACACAGAGGCGGAGTTTTGCAGTGAGT
                                                                                                                                                                                                                                                                                                                                                                             ATGCCTGTAATCCCAGCGCTTTGGGAGGCCGAGGCGGGTGGATCACTTCAGGTCAGGAGT 114251
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2001US-0286090P.
2001US-0292517P.
                              DNA;
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                              884
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Pred. No. 2.9e-
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                              59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            level of
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                                                                                                                                                                                                                                                                                                                                          The invention relates to the isolation of genes AAC78997-C79045 encoding CC 49 human secreted proteins AAB44335-B444382. The genes can be used to CC generate fusion proteins by linking to the gene for the human CC immunoglobulin GFc portion (AAC78988) for increasing the stability of the fusion protein as compared to the human protein only. The genes and CC proteins are useful for preventing, ameliorating or treating medical CC conditions, e.g. by protein or gene therapy. The genes are isolated from CC a range of human tissues disclosed in the specification. The nucleic CC diagnosis, roteins, antibodies and (anthagonists are useful in the CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and CC unarrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) CC immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, (e) interviews, autoimmune haemolytic cardiovascular disorders such as myocardial ischaemias; (d) wound healing (e) infectious diseases such as viral, bacterial, fungal and parasitic confectious diseases such as viral, bacterial, fungal and parasitic
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fourty nine nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulce vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disoneurological disease; infection; human; secreted protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein gene 13 clone HSREC72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-FEB-2001
                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-1999; 99US-0126602P
14-JAN-2000; 2000US-0176063P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2000; 2000WO-US007725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                               585
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                                                                                             CACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCATCCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 322; 367pp;
                                    CAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCATGGTGGCACA
                                                                                                                                               ATATTTTGTTTAAATGGAATCATACCAGGCTGGGCACAGTGCTCACGCCTGTAATCCTAG
CAATATGATGAAACCCCGTCTCTA-AAAAAATACAAAAATTAGCCGGGCGTGGTGTCAGG
                                                                      CACTTTGGGAGGCCAGGGTGGGCAGATCACCTGAGGTCGGGAGTTCGAGACCAGCCTGAC
                                                                                                                                                                                 AAATATTAATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCTGTAATCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                            BP; 211 A; 214 C; 226 G; 233 T; 0 U; 0 Other;
                                                                                                                                                                                                                                     38.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
                                                                                                                                                                                                                     <u>+</u>;
                                                                                                                                                                                                                     Score 153.6; DB 3
Pred. No. 9.2e-33;
1; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nootropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuroprotective; antiviral; antiinflammatory; antiulcer;
                                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                       70;
                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                             884;
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                                                                                                              156
                                        216
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     763
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Query Match
Best Local S
Matches 241
                                                                                                                                                                                                                            The present sequence encodes a beta-tubulin antigen. The protein is an antigen of the membranous structure of the inner ear protein, and is reactive with antibodies from patients having Meniere's disease.

Meniere's disease is a chronic ear disease with unknown etiology. Serum from patients suffering from this disease contain autoantibodies against a 30 kDa cochlear protein antigen. The disease is believed to be an autoimmune disease. The beta-tubulin antigen is useful as a target substance in diagnosing or detecting Meniere's disease and in
                                                                                                                                                                                                                                                                                                                                                                                                              New beta-tubulin antigen in the membranous structure of the inner ear, reactive with antibodies of patients with Meniere's disease, for diagnosing Meniere's disease and distinguishing this disease from othe
                                                                                                                                                                                  Sequence 14784 BP; 5454 A; 2966 C;
                                                                                                                                                                                                                 distinguishing
                                                                                                                                                                                                                                                                                                                                                                         Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                      diagnosing Meniere's disease autoimmune ear diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta-tubulin antigen; inner ear protein; Meniere's disease; autoantibody; chronic ear disease; autoimmune disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of a beta-tubulin antigen
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                              91
                                                                                          31 GAACCCAAATATTAATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCTGTAA
                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNIV TENNESSEE RES CORP
                                                                                                                                                                                                                                                                                                                                                                     Page 97-103; 115pp; English.
TCCCAGCACTTTGGGAGGCCAACGTGGGCAGATCACCTGAGGTCAGGAGTTCGAGACCAG
                            TCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCAT 150
                                                           GATCTAAGAATTTATTATAAAAGTGTAGCAAGGGCTGGGCGCGGGGCGCCTCACGCCTGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACCTGTAATCCCAGCTACTCAGGAAGCAGAGGTTGCAGTGAGCTGAGGTCG-----
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                                                                                                                        Conservative
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                                                                                                                                                                                                               disease from other autoimmune
                                                                                                                                     38.3%;
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                                                                                                                     Score 153.2; DB 3;
Pred. No. 2.9e-32;
0; Mismatches 128;
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                                                                                                                                                                                  T; 0 U; 0 Other;
                                                                                                                        Indels
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                       for use in evaluating the prognosis of patents suffering from acute myelogenous leukemia (AML) by analysis of the patients gene expression profile. The invention relates to a movel method for evaluating the prognosis of a patient with acute myelogenous leukemia by detecting higher/lower expression level of genes encoding mRNA recognized by a probe set chosen from 19 nucleotide sequences (AEE03340 or AEE03344-AEE03361). Also, gene expression profiling of AML patients using a set of probes based on 167 sequences (AEE03362-AEE03527) using a biochip was performed to determine prognosis. Methods are also included for determining an AML patient's state, determining AML patient's treatment protocol, determining whether the patient will respond to the treatment, and producing an AML patient's prognosis report by analysis of the patients gene expression profile. The methods are useful in evaluating an
                                                                                                                                                                                                                                                                                                                                               Evaluating an acute myelogenous leukemia patient's prognosis, comprisin detecting lower or higher expression level of gene recognized by probe set e.g. 202820-at and 206148-at, with respect to predetermined cut-off
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2006-004067/01
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                                                                                                                                                                                                                                                            The present sequence is that of a human gene sequence which is claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP2005333987-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEE03362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myelogenous leukemia; prognosis; gene expression;
                                                                                                                                                                                                                                                                                           NO 23; 60pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                  comprising
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REBUIT 16 ALC04559/c ID. AALC04559; AC AALC04599; AC AALC0	Sequence 166942 BP; 42646 A; 40900 C; 40852 G; 42544 T; 0 U; 0 Other; Duerry Match 38.2%; Score 152.8; DB 15; Length 166942; Best Local Similarity 75.0%; Pred. No. 7.8e-32; Matches 219; Conservative 1; Mismatches 63; Indels 9; Gaps 2; Db 33655 CCTATAATCCCAGCACTTTGGGAGGCCGAGGTAGATCACTTGAGGTCAAGAGTTCG Oy, 144 AGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAATACTGGTGG 33714 Oy, 144 AGACCAGCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAAAAA
**************************************	\$\frac{1}{2} \times \frac{1}{2}
12-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 21-SEP-2000; 21-SEP-2000; 22-SEP-2000; 23-SEP-2000; 29-SEP-2000; 29-CCT-2000; 29-CCT-2000; 29-CCT-2000; 29-CCT-2000; 29-CCT-2000; 20-CCT-2000; 20-CC	14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 11-AUG-2000; 22-AUG-2000; 22-AUG-2000; 23-AUG-2000; 23-AUG-2000; 30-AUG-2000; 30-AUG-2000; 01-SEP-2000;
2000US-023196P- 2000US-023239PP- 2000US-023239PP- 2000US-0232340PP- 2000US-023340PP- 2000US-023340PP- 2000US-023340PP- 2000US-023340PP- 2000US-02349PPP- 2000US-023549PP- 2000US-023549PP- 2000US-0235336P- 2000US-0235336P- 2000US-0235336P- 2000US-0235336P- 2000US-0235338P- 2000US-023538PP- 2000US-023538PP- 2000US-023538PP- 2000US-023538PP- 2000US-023538PP- 2000US-023538PP- 2000US-0237039P- 2000US-0237039P- 2000US-0237039P- 2000US-0237039P- 2000US-023703PP- 2000US-023703PP- 2000US-024186PP- 2000US-0241786PP- 2000US-0241786PP- 2000US-0244178PP- 2000US-024417PP- 2000US-0244677PP- 2000US-0246477PP- 2000US-024647PP- 2000US-024647PP- 2000US-024647PP- 2000US-0246524P- 2000US-0246525P- 2000US-0246525P- 2000US-0246527P- 2000US-0246527P- 2000US-0246527P- 2000US-0246527P- 2000US-0246527P- 2000US-0246527P- 2000US-0246527P- 2000US-0246527P-	NUS - 0225270 NUS - 0225757 NUS - 0225757 NUS - 0225758 NUS - 0225758 NUS - 0226681 NUS - 0226681 NUS - 0226681 NUS - 022708 NUS - 022708 NUS - 0229243 NUS - 0229344 NUS - 0229345 NUS - 0231243

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                                                                                                                                                                                           The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be use in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding protein of the invention
                                                                                                                                                                        Sequence 4388 BP;
                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                            Isolated nucleic acid molecule encoding a reproductive system ant used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                       Rosen
                                                                                                                                                                                                                                                                                                                                                           (HUMA-)
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17-NOV-2000;
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                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                           HUMAN GENOME
                                                                                              ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                     TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAAATACAAAAAAATAGC
                                        TCGAGACCAGCCTGGCCAACATGGTGAAACTCCGTCTCTACTAAAAATTACAAAAATTAGC
                                                                                   AAGCCTGTAATTCCAGCACTTTGGGAGGCCGAGGCCGGCGGATCACTTGAGGTCAGGAGT
            TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGC
CGCACGTGGTGGCGCGCGCCTGTAATCCCCAGCTACTCGGGAGGCGGAGGTTGCAGCGAGC
                                                                                                                                                                                                                                                                                                                                      Barash
                                                                                                                                                                                                                                                          SEQ ID NO 7647; 1297pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0246610P
2000US-0246611P
2000US-0246611P
2000US-0249209P
2000US-0249210P
2000US-0249211P
2000US-02511868P
2000US-02511868P
                                                                                                                              Conservative
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2000US-0246532P.
2000US-0246609P.
                                                                                                                                                                                                                                                                                                                                      SC,
                                                                                                                                                                   870 A; 1238 C; 1205 G; 1075 T; 0 U; 0 Other;
                                                                                                                                      38.1%;
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                                                                                                                                                                                                                                                                                                                                      Ruben
                                                                                                                           1;
                                                                                                                            Score 152.4; DB 4;
Pred. No. 3.3e-32;
1; Mismatches 52;
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                                                                                                                                               Length
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RESULT 17
ABL57853/c
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AC ABL57853;
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XX
Human; test
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Human; tes
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26-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
16-AUG-2000;
17-AUG-2000;
18-AUG-2000;
19-AUG-2000;
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28-JUN-2000;
30-JUN-2000;
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17-MAR-2000;
18-APR-2000;
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02-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; DNA; 4388
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2000US-0225759P
2000US-022681P
2000US-022688P
2000US-022688P
2000US-02271082P
2000US-0227099
2000US-0228924P
2000US-02289287P
2000US-0229343P
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2000US-0190076P
2000US-0205515P
2000US-0205515P
2000US-0214886P
2000US-0214880P
2000US-0216880P
2000US-0217487P
2000US-0217487P
2000US-0218290P
2000US-0224518P
2000US-0224518P
2000US-0225114P
2000US-0225264P
2000US-0225264P
2000US-02252451P
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2000US-0225264P
2000US-0225247P
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2000US-0186350P
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08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 12-SEP-2000;

2000US-0229509P.
2000US-0229513P.
2000US-023043PP.
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2000US-0231243P.
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2000US-0231414P.
2000US-0231414P.
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2000US-0232397P.

05-SEP-2000; 05-SEP-2000; 06-SEP-2000; 06-SEP-2000;

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                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic
                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 2505; 766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        preventing,
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                                                                                                                                                                                                                                                                                            fragment
                                                                                                                                                                                                                                                                                                                                                                                                                    acids encoding
                                          TCGAGACCAGCCTGGCCAACATGGTGAAACTCCGTCTCTACTAAAAATACAAAAATTAGC
                                                                                                                                              TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAAATAGC
                                                                                                                                                                                                                                                                     4388 BP;
            CAAAAACAACAACAAAAAACAAAA
                                                                                      TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                               AAGCCTGTAATTCCAGCACTTTGGGAGGCCGAGGCCGGCGGATCACTTGAGGTCAGGAGT
                                                                                                                                                                                           ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
38.1%;
nilarity 76.5%;
Conservative
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2000US-0249211P

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2000US-0249299P

2000US-0249299P

2000US-0250391P

2000US-0251030P

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2000US-0251866P

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                                                                                                                                                                                                                                                                                                                                                                                                        diagnosing
                                                                                                                                                                                                                                                                                            of the invention
                                                                                                                                                                                                                                                                    870 A; 1238 C; 1205 G; 1075 T;
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                                                                                                                                                                                                                                                                                                                                                                                                        human testicular antigen polypeptides, and/or treating testicular cancer.
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                                                                                                                                                                                                                          Score 152.4; DB 4;
Pred. No. 3.3e-32;
1; Mismatches 52;
 1021
                      344
                                                                                                                                                                                                                                                                       0 U; 0 Other;
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14-SEP-2000;
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26-SEP-2000;
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20-CCT-2000;
20-CC

2000US-023298P 2000US-023239P 2000US-023239P 2000US-023239P 2000US-023363P 2000US-023363P 2000US-023363P 2000US-023423P 2000US-023423P 2000US-023423P 2000US-0235834P 2000US-0235834P 2000US-0235834P 2000US-023637P 2000US-02478P 2000US-02478P 2000US-02478P 2000US-024677P 2000US-0249217P 2000US-0249217P 2000US-0249217P 2000US-0249217P

RESULT 18 ABL68122/c ID ABL68122 standard; DNA; 174424 BP

ABL68122;

15-MAY-2002

(first entry)

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28-SEP-2000
29-SEP-2000
29-SEP-2000
02-OCT-2000
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03-OCT-2000
03-OCT-2000
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03-OCT-2000
03-OCT-2000
Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
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28-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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                                                                                                              (AVAL-) AVALON PHARM.
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                                                                           Augustus M, Weaver Z;
                                                                                                                                  2000US-0235280P
2000US-0235633P
2000US-0235711P
2000US-0235840P
2000US-0235863P
2000US-0236032P
2000US-0236033P
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2000US-0209531P.
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26-NOV-2002; 2002US-0429739P.

(PROT-) PROTEIN DESIGN LABS INC

26-NOV-2003; 2003WO-US038193

Homo sapiens.

WO2004048938-A2

LO-JUN-2004.

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ARESULT 19
ADQ19573/c
ID ADQ195
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XX BOFT 26-AUG
DT 26-AUG
DX Human
XX BOFT t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL7010), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC rumour.
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Best Local
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ds.
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RESULT 20
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                                                                                                                                                                                                                                                                                                                                        Human; osteoblast; stem cell differentiation;
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                                                                                                                                                                                                                                                                                                                                                                                                             differentiation related cDNA SEQ ID
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Pred. No. 1.3e-31;
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RESULT 21
AAK68418/c
ID AAK684
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AC AAK684
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DT 06-NOV

standard; DNA; 14282

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06-NOV-2001 AAK68418; AAK68418

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to genes and their expression profiles are used for: (a) screening modulators of precursor stem cell differentiation i osteoblasts, or bone tissue deposition; (b) diagnosing abnormal deposition of bone tissue, abnormal rate of osteoblast formation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of genes and their expression profiles associated with osteoblast differentiation for screening modulators bone formation, for diagnosing or treating e.g. osteoporosis, or as markers for the differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-2000; 2000US-0255882P.
24-APR-2001; 2001US-0285691P.
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PROCTER & G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                              GGTAAGAAAATCTTAGTTAAAGATCTAAAGTTTGGCCAGGCACAGTGGCTAACGCCTGTA 125833
                                                                                                                                                                                                                                                                                                                                                                                                           GGAACCCAAATATTAATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCTGTA
                                                                                                                                                                                                                                                   TCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCATGG 209
                                                                                                                                                                                                                                                                                                    ATCCCAGCACTTCGGGAGGCCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTCGAGACCA 125773
                                                                      TGGGTGAGTCAAGATCGCAACATGGCACTCCAGCCTGGGCAACAGAGACTCCATCTCCAA 12559
                                                                                                                                                                        TGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAGATCGC 269
                                                                                                                                                                                                                         GCCTGGCCAACATGGTGAAACCCCTGTCTCTACTAAAAATTACAAAAATTAGCCGGGCATGG
                                                                                                                                                                                                                                                                                                                         ATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCA 149
                                                                                                               AGAGTGAGCCGAAATCACA----GATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAAA 324
AAAAATAAATAAATAAAAATAA 125571
                                   ААСААСААСААААААСАААААА 347
                                                                                                                                                   TGGCAGACACCTGTAGTCCCAACTACTCAAGAGGCTGAGGCAGGAGAATCACTTGAAC-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 151.4; DB 6;
Pred. No. 1.9e-31;
1; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35660 C; 35715 G; 48555 T; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           <del>ن</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       89
                                                                                                                                                      125654
                                                                                                                                                                                                                                 125713
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12 4-FEB-20001, 2000US-0184564P. 12 4-MR-20001, 2000US-0184556P. 11 4-MR-20001, 2000US-0198128P. 11 4-MR-20001, 2000US-0198128P. 11 4-MR-20001, 2000US-0198128P. 12 4-MR-20001, 2000US-0198128P. 13 -MR-20001, 2000US-011688P. 14 -MR-20001, 2000US-011688P. 15 -MR-20001, 2000US-011688P. 16 -MR-20001, 2000US-011489P. 11 -MR-20001, 2000US-0125518P. 14 -MR-20001, 2000US-012556P. 14 -MR-20001, 2000US-012556P. 14 -MR-20001, 2000US-0125579P. 14 -MR-20001, 2000US-0125579P. 14 -MR-20001, 2000US-0125579P. 14 -MR-20001, 2000US-0125579P. 14 -MR-20001, 2000US-012559P. 20 -MR-20001, 2000US-012559P. 20 -MR-20001, 2000US-012559P. 20 -MR-20001, 2000US-012559P. 20 -MR-20001, 2000US-01259P. 20 -MR-20001, 2000US-013144P. 20 -MR-20001, 2000US-013144P. 20 -MR-20001, 2000US-013149P. 20 -MR-20001, 200US-013149P. 20 -MR-20001, 2000US-013149P. 20 -MR-20001, 2000US-01	-JAN-2001; 2001WG-0300135 -JAN-2000; 2000US-0179065 -FEB-2000; 2000US-0180628	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23230. Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds. Homo sapiens. W0200157182-A2. 09-AUG-2001. 17-JAN-2001; 2001WO-US001354.
	PR PR	קר אי קר קר קר קר אי אי אי אי א אי א אי
	9-SEP-2000; 2-OCT-2000; 2-OCT-2000; 2-OCT-2000;	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
2000US-0237039P 2000US-0237039P 2000US-0239937P 2000US-0239937P 2000US-0241221P 2000US-0241221P 2000US-02411808P 2000US-0241809P 2000US-0241809P 2000US-0241809P 2000US-0246677P 2000US-0246677P 2000US-0246677P 2000US-0246677P 2000US-0246677P 2000US-0246675P 2000US-0246675P 2000US-0246623P 2000US-0246611P 2000US-0246611P 2000US-0246611P 2000US-0246611P 2000US-0249207P 2000US-0249211P 2000US-024921P 2000US-0255166P 2000US-0251866P 2000US-0251866P	0000	

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RESULT 22
AAS28363/c
ID AAS283
XX
AC AAS283
XX
DT 07-NOV
XX
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Genomi
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XX
KW Human;
KW lung d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARKS4951 to ARK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in ARM62170 to ARM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynuclectides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynuclectides may be used to produce the secreted (II, by inserting the CC protein. (I) proteins and polynuclectides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic concerns and cancer metastases of haematopoietic antigen genomic concerns from the present invention. ARK54992 to ARK64703 and AAM62169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
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08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 23230; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-483426/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA,
Human; respiratory antigen; respiratory disorder; throat disorder; lung disorder; nose disorder; lung cancer; gene therapy; cytostatic;
                                              Genomic sequence #203 encoding for novel human respiratory antigen.
                                                                                  07-NOV-2001
                                                                                                                 AAS28363;
                                                                                                                                              AAS28363 standard; DNA; 32146 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14282 BP; 3993 A; 2449 C; 2814 G; 5026 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match
                                                                                                                                                                                                                                                                                            4604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4784 AAATAATGTTATCCTGGCCAGGCACGGGGCCACATGCCTGTAATCCCAGCACTTTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                         168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192;
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                                                                                                                                                                                                                                GGGCAACAGAGTGAACTCTGT 4524
                                                                                                                                                                                                                                                                                            CCAGCTACTGAGGAGGCAGAGGTTGCAGTGAGCCGAGATCACACCCACTGCATTCCAGCCT 4545
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCATCCTGGCCAACATGGTGA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCTGTAATCCCCAGCACTTCGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                          ACCGAGGTGGGCAGATCACTTGAGGTCAGGAGTTTGAGGCCAGCCTGGCCGACATGGTAA
                                                                                                                                                                                                                                                   AGATCACAGAGTGAGCAGAGT 308
                                                                                                                                                                                                                                                                                                                                                                                          AACCCCGTCTTTACTAAAAATACAAAAATAGCTGGGCATGGTGGCACACCCTGTAGTC
                                                                                                                                                                                                                                                                                                                           CCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATCAC
                                                                                                                                                                                                                                                                                                                                                           AACCCCGTCTCTACTAAAAATAAAAAATTAGCTGGGTGTCGTGGCATGCACCTATAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 150.6; DB 4
Pred. No. 1.5e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 14282;
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                                                                                                                                                                                                                                                                                                                                                                                       227
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      08-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
12-SEP-2000;
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01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
30-AUG-2000;
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28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
                                                14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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14-SEP-2000;
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14-SEP-2000;
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18-AUG-2000;
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14-AUG-2000;
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14-AUG-2000;
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14-AUG-2000;
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14-AUG-2000;
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14-AUG-2000;
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14-JUL-2000;
26-JUL-2000;
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respiratory active; ds.
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11-JUL-2000;
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16-MAR-2000;
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01-SEP-2000;
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                                 2000US-022570P

2000US-0225747P

2000US-02257579P

2000US-0226881P

2000US-0226881P

2000US-0226881P

2000US-0227182P

2000US-0227182P

2000US-0229343P

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2000US-0232398P

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2000US-02333064P

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2000US-0225213P.
2000US-0225214P.
2000US-0225266P.
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2000US-0190076P.
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2000US-0225268P.
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음 성

В 5 음 성

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prognosing respiratory cancers

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25-SEP-2000; 2000US-0234997P
25-SEP-2000; 2000US-0235484AP
27-SEP-2000; 2000US-0235484AP
27-SEP-2000; 2000US-023536P
29-SEP-2000; 2000US-023636P
29-SEP-2000; 2000US-023636P
29-SEP-2000; 2000US-023636P
29-SEP-2000; 2000US-0236370P
29-SEP-2000; 2000US-0236370P
29-SEP-2000; 2000US-0236370P
29-SEP-2000; 2000US-0237039P
29-CCT-2000; 2000US-02393703P
29-CCT-2000; 2000US-023933P
29-CCT-2000; 2000US-023933P
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20-CCT-2000; 2000US-02341785P
20-CCT-2000; 2000US-02341787P
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20-CCT-2000; 2000US-02411809P
20-CCT-2000; 2000US-02411809P
20-CCT-2000; 2000US-02411809P
20-CCT-2000; 2000US-02411809P
20-CCT-2000; 2000US-024617P
20-CCT-2000; 2000US-024617P
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20-CCT-2000; 2000US-0246474P
20-CCT-2000; 2000US-0246474P
20-CCT-2000; 2000US-0246474P
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20-NOV-2000; 2000US-0246610P
20-NOV-2000; 2000US-0246528P
20-NOV-2000; 2000US-0246528P
20-NOV-2000; 2000US-0246529P
20-NOV-2000; 2000US-0246529P
20-NOV-2000; 2000US-0246529P
20-NOV-2000; 2000US-0249218P
217-NOV-2000; 2000US-0249219P
217-NOV-2000; 2000US-024929P
217-NOV-2000; 2000US-024929P
217-NOV-2000; 2000US-024929P
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217-NOV-2000; 2000US-024929P
217-NOV-2000; 2000US
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ID ADG415
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AC ADG415
XX DT 26-PEB
XX AG Human
XX Antiin
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KW human
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Best Local Similarity
Matches 224; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the isolation of novel human respiratory antigens (AAU17685-AAU17975), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing disorders related to the respiratory system including throat disorders (e.g. vocal cord paralysis, consilittis, and laryngitis), lung disorders e.g. pneumonia, allergic disorders e.g. asthma, pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of the respiratory tissues e.g. lung cancer. The polymucleotide sequences of the invention are useful in gene therapy and antisense therapy. AAS28161-AAS28764 represent genomic sequences encoding for novel human respiratory antigens. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
  antiinflammatory; antiallergic; antiasthmatic; cytostatic; gene therapy;
respiratory system antigen;
human respiratory system associated polynucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide for treating, preventing and/ or disorders related to the respiratory system including and also for testing and detection e.g. diagnosis.
                                                                                       Human respiratory system associated
                                                                                                                                                                                                                             ADG41559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 32146 BP; 8745 A; 6747 C; 7148 G;
                                                                                                                                        26-FEB-2004
                                                                                                                                                                                   ADG41559;
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                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                 CCCAGACTATTGCAGGAGACCAAAAAG 400
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                                                                                                                                                                                                                                                                                                                                                                                                                               TCCGTCTCMAAAAAAAAAAAAAAAAAAAAAAAAAAGTAGAGACAATAGGGGGA
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2138 373 2198 313 2258

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m disorder; throangitis; lung disorder; throangitis; lung disorder; lung disorder; lung disorder; lung disorder; lung disorderis; lung disorde
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2000US-0233063P 2000US-0233064P 2000US-0233064P 2000US-0234223P 2000US-02342349P 2000US-0234998P 2000US-0235368P 2000US-0235369P 2000US-0235369P 2000US-0235369P 2000US-0235369P 2000US-02353703PP 2000US-02353703PP 2000US-02353703PP 2000US-02363703PP 2000US-02363703PP 2000US-02363703PP 2000US-02363703PP 2000US-02341785P 2000US-02341785P 2000US-02441787P 2000US-02441787P 2000US-02446179P 2000US-0244617PP 2000US-0244617PP 2000US-0244617PP 2000US-0244617PP 2000US-0244617PP 2000US-0244617PP 2000US-0244617PP 2000US-0244611PP 2000US-0244211PP 2000US-0244211PP 2000US-0244211PP 2000US-0244221PP 2000US-02
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The invention describes an isolated polypeptide (I) comprising an amino CC acid sequence that is at least 90% identical to polypeptide fragment of any one of 299 respiratory system antigen sequences (PS) and having CC biological activity, polypeptide domain or epitope of PS, (II)-length (II) encoding (I) is also useful for diagnosing a CC pathological condition or a susceptibility to a pathological condition or a susceptibility to a pathological condition of in (II) or determining the presence or absence of mutation CC in (II) or determining the presence or amount of expression of (I) in a CC diagnosing a pathological sample and diagnosing a pathological condition based on the CC diagnosic are useful in diagnosis. Treatment, prevention and/or CC diagnosis of disorders of respiratory system associated polynucleotides, the prognosis of disorders of respiratory system such as throat disorders (e.g., pneumonia), altergic disorders (e.g., asthma and ecsinophilic sarcoidosis, nose disorders (thinitis and sinusitis), neoplasms and/or cancers of respiratory tissues (e.g., asthma and ecsinophilic sarcoidosis, nose disorders (thinitis and sinusitis), neoplasms and/or cancer of the nose). The polynucleotides are useful in gene therapy techniques, for chromosome identification, identifying individuals from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0254678P.
17-JAN-2001; 2001US-00764860.
14-FEB-2002; 2002US-00074095.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
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TCTCAGCAAATACTGGATTTAACAAAG 2111
                                                                                                  CCCAGACTATTGCAGGAGACCAAAAAG 400
                                                                                                                                                                                                           TCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAGATAAAAGTAGAGACAATAGGGGGA
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07-JUN-2000

17-MAR-2000;

2000US-0184664P. 2000US-0186350P. 2000US-0179065P. 2000US-0180628P.

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14-AUG-2000; 18-AUG-2000; 18-AUG-2000; 22-AUG-2000; 22-AUG-2000; 23-AUG-2000; 31-AUG-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 05-SEP-2000; 06-SEP-2000; 06-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000;

14-AUG-2000; 14-AUG-2000; 14-AUG-2000;

2000US-0189874P.
2000US-0198123P.
2000US-0198123P.
2000US-0214886P.
2000US-0214886P.
2000US-0214886P.
2000US-021488P.
2000US-021513P.
2000US-0217487P.
2000US-0224518P.
2000US-0224518P.
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2000US-0225213P.
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RESULT 24
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08-SEP-2000; 08-SEP-2000; 12-SEP-2000; 14-SEP-2000; 14-SEP-2000;

14-SEP-2000; 14-SEP-2000;

2000US-0232401P. 2000US-0233064P. 2000US-0233065P. 2000US-0233065P. 2000US-0234273P. 2000US-0234274P. 2000US-0234274P. 2000US-0234298P.

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06-DEC-2000
08-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention is related to a novel isolated polypeptide, which comprises a human respiratory system-related polypeptide, and the DNA sequence which encodes it. The invention may be useful for the development of compounds with an antiasthmatic, antibacterial, antiinflammatory, cytostatic, antianaemic or antiallergic activity. In addition, the sequences disclosed may be useful for gene therapy. The polypeptide or polynucleotide is useful for treating, preventing or ameliorating a medical condition, for example pneumonia, lung cancer, cystic fibrosis, asthma, sarcoidosis, rhinitis, anaemia, leukaemia, inflammations, sinusitis, chronic obstructive pulmonary disease or infectious diseases. The polypeptide or polynucleotide is also useful for diagnosing any of these diseases or a susceptibility to the disease. The present sequence is that of a human DNA sequence which is related to a human reservier or vertem associated cone of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human respiratory system-related polypeptide and genes, useful treating, preventing or diagnosing e.g. pneumonia, lung cancer, cys fibrosis, asthma, sarcoidosis, rhinitis, leukemia, inflammations or
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
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                                                                                                                                                                                                                                                                                                                                                            Local Local 224;
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2137
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                                                                                                                                                                                                      TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAG------CCGGAGATTGC
                                                                                                                                                                                                                                                                TCGAGACCATCCTGGCCAACATGGTGAAACCCCGGTCTTTACTAAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                    32146 BP; 8745 A;
 TCTCAGCAAATACTGGATTTAACAAAG
                                                           TCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAGATAAAAGTAGAGACAATAGGGGGA
                                                                                        KCCGTCTCAAAAACAACAACAAAAAAACAAAAAAACCATAAGACATTGTCCATCTGCGGTT
                                                                                                                                                     AGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGAC
                                                                                                                                                                                                                                                TTGAGACAAGCCTGGCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAATTAGC
                                                                                                                                                                                                                                                                                                             ACGCCTGTAATGCTAGCACTTTGGGAGGCCAAGGCGGGGGGTCACTTGAGGTCAGGAGT
                           CCCAGACTATTGCAGGAGACCAAAAAG 400
                                                                                                                       CTTGAACCCGGGAGGCGGAGGTTGCAATGAGCCGAGATTGTACTACTGCAATGCAGAGAC
                                                                                                                                                                                    AGGGCATGGTGGCGGGCACCTGTAGTCCCAGCTGCTTGGGAGACTGAGCCAGGAGAATTG
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2000US-0250391P.
2000US-025198BP.
2000US-0251798BP.
2000US-0251479P.
2000US-0251866P.
2000US-0251869P.
2000US-0251869P.
2000US-0251989P.
2000US-0251989P.
2000US-0254999P.
2000US-025499P.
2001US-0259678P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 797; 202pp; English.
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                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                         Score 150.6; I
Pred. No. 1.9e-
1; Mismatches
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es 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                      9506 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                      DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the invention.
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Length 32146;
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cystic
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2000US-0235834P.
2000US-023633P.
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2000US-0237037P.
2000US-0237034P.
2000US-0247036P.
2000US-0241785P.
2000US-0241786P.
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2000US-0241786P.
2000US-0241786P.

14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
20-CCT-2000;
20-CC

2000US-0241826P 2000US-024647P 2000US-024647P 2000US-024647P 2000US-024647P 2000US-0246523P 2000US-0246528P 2000US-0246528P 2000US-0246528P 2000US-0246528P 2000US-0246528P 2000US-0246528P 2000US-0246532P 2000US-0246611P 2000US-0246611P 2000US-0246611P 2000US-0246611P 2000US-0249619P 2000US-024921P 2000US-024924P 2000US-024924P 2000US-024924P 2000US-024924P 2000US-024924P 2000US-024924P 2000US-024924P 2000US-024924P 2000US-024929P 2000US-024929P 2000US-024929P

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RESULT 25
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AC ADL139
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Best Local Similarity
Matches 202; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining susceptibility of an individual to joint space narrowing, osteophyte development and/or joint pain comprises identifying whether the individual has at least one polymorphism in a polymucleotide encodition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 125515 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a procein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             osteoarthritis; SNP; single nucleotide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ds; gene; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Osteoarthritis-associated polymorphic nucleotide #473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-2004 · (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL13941;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention individual to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2003-559141/52
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                                                                                                                                                                                                                                                                                         ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                             TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                     ATGCTTGTAATCCCAGCACTTTGGGAGGCTGAGGAGGGCGGATTATTTGAGGTCAGGAGT
                                                       TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schafer A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ
                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
rggtggcacgcacctgtagtcccagctgctcaggagacacaggttgcagtgagc
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                                                                                                                                                                                                                                                                                                                                                                                                        37.7%;
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osteophyte development; joint pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297pp; English
                                                                                                                                                                                                                                                                                                                                                                        Score 150.6;
Pred. No. 3e-3
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U; 0 Other;
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21-JUL-1998;
22-DEC-1998;
                                                 The present sequence is a gene encoding human myelin oligodendrocyte glycoprotein which is a nervous system-specific antigen. The antigen or peptides derived from it activate T cells in vivo. The present sequence is used to promote nerve regeneration or to prevent or inhibit neuronal degeneration caused by injury or diseases of nerves within the CNS or PNS. Such injury includes spinal cord injury, blunt trauma, penetrating trauma, haemorrhagic stroke or ischaemic stroke, whilst diseases include diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
                          Human; myelin oligodendrocyte glycoprotein; MOG; NS-specific antigen; nervous system-specific antigen; T cell; peripheral nervous system; PNS central nervous system; CNS; nerve regeneration; neuronal degeneration;
                                                                                                                                                                               Claim
                                                                                                                                                                                                       New compositions useful to treat nervous system traumatic injury, Alzheimer's disease etc.
                                                                                                                                                                                                                                                                                          Eisenbach-Schwartz M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spinal cord injury; blunt trauma; penetrating trauma; senile dementia;
ischaemic stroke; diabetic neuropathy; glaucoma; haemorrhagic stroke;
Alzheimer's disease; Parkinson's disease; Huntington's chorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human myelin oligodendrocyte glycoprotein gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ29204
                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amyotrophic lateral sclerosis; ALS; treatment;
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MCINNIS P A.
                                                                                                                                                                             Fig 18;
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                                                                                                                                                                                                                                                                                                                                                              98IL-00124550.
98WO-US014715.
98US-00218277.
                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US010953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= "myelin oligodendrocyte glycoprotein"
/pote= "Reading frame is interrupted by introns
precise location of which is not given in the
                                                                                                                                                                           92pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                             English.
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                                        lateral sclerosis,
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                                                                                                                                                                                                                        disease
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Sequence 17538

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Best Local
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22-DEC-1998;
19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS; central nervous system; peripheral nervous system; tranquillizer; MOG; vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant; nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic; osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy, myelic nitralarization.
The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering
                                                                                                                                                                 central/peripheral nervous administering nervous syste analogs/peptides.
                                                                                                                                                                                              Promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or
                                                                                                                                                                                                                                                                                                                                                                                                   Moalem
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eisenbach-Schwartz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUN-2001; 2001US-00893348.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human myelin oligodendrocyte glycoprotein (MOG) gene sequence.
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DB; ABB81071.
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                                                                                                            Fig 18; 93pp; English.
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98WO-US014715.
98US-00218277.
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Pred. No. 1.8e-31;
0; Mismatches 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC damages caused by surgery such as tumour excision. The disease is not an CC autoimmune disease or neoplasm. The disease results in a degenerative CC process occurring in either gray or white matter or both. The disease is CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and CC vitamin deficiency, intervertebral dise herniation, prion diseases such as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral CC neuropathies associated with various diseases, including but not limited CC to uremia, popphyria, hypoglycemia, Sjorgren Larsson syndrome, acute CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary camploidosis, obstructive lung diseases, acromegaly, malabsorption CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-CC pathies, complications of various drugs (e.g., metronidazole) and toxins CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia telangectasia, Friedreich's ataxia, amyloid polyneuropathies, Fabry's CC disease, or lipoproteinemia. The present sequence represents a human of compandors of the present sequence represents a human of the compandors of the present sequence represents a human of the compandors of the present sequence represents a human of the compandors of the present sequence represents a human of the compandors of the present sequence represents a human of the compandors of the present sequence represents a human of the compandors of the present sequence and toxins of the compandors of the present sequence and toxins of the compandors of the present sequence and toxins of the compandors of the present sequence and the compandors of the compando
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17538 BP; 4624 A; 4120 C; 3991 G; 4803 T;
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                                                      САААААСААСААСААААААСААЛАЛААССАТА
                                                                                                                                                                  TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                                                                                                                              TGGGCATGGTGGCATGCGCCTGTAGTTCCAGCAACTTGGGAGGCTGAGGCAGGAGAATCG 13349
                                                                                                                                                                                                                                                                                                                                                TCAAGACCAGCCTGGCCAACATGGTGAAACCCCCGTCTCTACTAAAAAATACAAAAATTAGC
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72.1%;
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Pred. No. 1.8e
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RESULT 28
ADQ97695/c
ID ADQ97695 standard; DNA; 88892 BP.

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ADQ97695;
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ADQ97695;
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DT 07-OCT-2004 (first entry)
XX
DE Human cancer associated sequence HD10-029, SEQ ID 672.
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Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human; ds
XX
PN WO2004060304-A2.
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PN WO2004060304-A2.
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PD 22-JUL-2004.
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22-DEC-2003; 2003WO-US041389.
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Best Local S
Matches 204
                                                                                                                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; cheropathy; central nervous system; CNS; Alzheimer's, Parkinson's disease, Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                            26-JUL-2001.
                                                                                                                  WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polymucleotide SEQ ID NO 5031.
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74.5%;
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Pred. No. 3e-
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26-DEC-2000; 2000WO-US034263

RESULT 30 AED18472

AED18472

standard;

DNA;

100998

BXAXAXI

15-DEC-2005

(first entry)

Fibrotic disorder associated polynucleotide SEQ ID

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Best Local
                                                                                                                                                                                                                                                                                                                       immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang
Wang
Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids and polypeptides, useful as central nervous system injuries.
                                                                                                                                                                                                                                                                                                Sequence 4779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 5031; 10078pp; English.
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03-AUG-2000;
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20-JUN-2000;
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21-JAN-2000;
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177; Conserv
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Wang Z,
Goodrich
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CGAGATTGCGCCACTGCACTCCAGCCTGGGCGACACAGTGAG
                                                                              TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                  TCAAGACCAGCCTGGCCAACATGGTGAAACCCCCATCTCTACTAAAAAATACAAAAATTAGC
                                                                                                                                               TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
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                          TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAG
                                                         TGGGCGTGGTGGCACATGCCTGTAGTCCCAGCTATTTGGGAGGCTGAGGCTGCAGTGAGC
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2000US-00488725.
2000US-00552317.
2000US-00598042.
2000US-00620312.
2000US-00623450.
2000US-00662191.
2000US-00662191.
2000US-0062344.
                                                                                                                                                                                                                                       Conservative
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Wehrman T,
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79.7%;
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Xue AJ,
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Yang
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Zhang J,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with a test agent, and determining if the test agent modulates the expression of the gene or biological activity of the polypeptide encoded by the gene. Also described are: detecting a fibrotic disorder in a subject; modulating gene expression in fibrotic tissue; and an array comprising a substrate having addresses, where each address has a capture probe that can specifically bind at least one polymucleotide that is differentially expressed in fibrotic disorders, or its complement. The method is useful in identifying a modulator of at least one gene that is differentially-expressed in fibrotic tissue or during fibrogenesis, or a differentially-expressed in fibrotic tissue or during fibrogenesis, or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiinflammatory; gene therapy; therapeutic; diagnosis; uterine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide encoded by the differentially-expressed gene, in a cell population for preparing a composition for diagnosing or treating fibrotic disorders, e.g. uterine fibrosis. This sequence represents a polynucleotide associated with detection and treatment of fibrotic disorders. Note: This sequence does not appear in the printed specification but has been obtained in electronic format directy from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a method of identifying a modulator of at least one gene that is differentially-expressed in fibrotic tissue or during fibrogenesis, or a polypeptide encoded by the differentially-expressed gene, in a cell population, comprising contacting the cell population with a test agent, and determining if the test agent modulates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying a modulator of a gene that is differentially-expressed in fibrotic tissue or during fibrogenesis, or a polypeptide encoded by the gene, in a cell population by contacting the cell population with a test
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19-OCT-2004; 2004US-0620444P.
15-DEC-2004; 2004US-0636240P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 100998 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-703565/72.
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93164
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                                   TGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAGATCGC
                                                                                                                           GCCTGGCCAACATGGTGAAACCCCTGTCTCTACTAAAAGTACAAAAATCAGCCAGGCATGG
TGGCAGGCGCCTGTAATCCCAGCTACTCGGGAGGCTGAGAATCACTTGAACCCTGGAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Pred. No. 4.1e-31;
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fibroids; gynecological; inflammation;
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liver cirrhosis; fibrosis; hepatoma; SNP detection; CABIN1; ds.
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Qy 84 CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG 143	Query Match 37.5%; Score 149.8; DB 14; Length 151909; Best Local Similarity 71.0%; Pred. No. 5.2e-31; Matches 211; Conservative 1; Mismatches 83; Indels 2; Gaps 1;	9.0	variation 122339	FT /*tag= bn FT /standard_name= "Single nucleotide polymorphism" FT variation 120523 FT /*tag= bi	variation 120210	r variation 118132	FI /"Lag= De FT /standard_name= "Single nucleotide polymorphism" FT variation 117729	variation 117478	variation (17399	variation /standar	FT variation 110228 FT variation 1.0228 FT variation 1.0228	variation /standar	variation /standard	variation	variation 103205	variation 102545	2	variation 98461	variation 97080	/standard variation 96770 /*tag= a	variation /standard /*tag= a	variation	FT /*tag= ao FT variation 95508 FT /*tag= an

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Matches 196; Conservative
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                                                                                                                                                                 The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for treating carcinoma; (vi) for inhibiting the activity of CAP; (vi) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma are propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent useful as patent is an equivalent to basic patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genomic
                                                                                                                        Sequence 196686 BP; 53978 A; 42758 C; 43862 G; 55372 T; 0 U; 716 Other;
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL65836 standard;
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18-SEP-2000;
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reconfiastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL6164 (to ABL70110), or is at least 95% identical to (S), where a change in comprises a sequence of anti-neoplastic activity. (I) has cytostatic expression is indicative of anti-neoplastic activity. (I) has cytostatic cativity and can be used in gene therapy. MI can be used for screening an expression is the data is sufficient to convey the chemical structure and/or of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, concer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cancer, infiltrating lobular cancer, squamous cancer, infiltrating neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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02-OCT-2000;
02-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 4173; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening for anti-neoplastic agent involves exposing cells to a agent to be tested for anti-neoplastic activity, and determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-188264/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression of a gene of a signature gene set
                                                                                          5127
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DR,
                                                                                                                                    263
                                                                                                                                                                                                                                                                                                                      143
                                                                                                                                                                                                                                                                                                                                                                                                                                                          201;
                                                                                                                                                                                                                                                                                                                                                                                                             83
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                                                                                                                                                                                                                GGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTG
                                                                                                                                                                                                                                                                      AAGACCAGTCTGGCCAACATGGTGAAACCCCCGCCTCTACTAAAAATACAAAATTAGCTG
                                                                                                                                                                                                                                                                                                        GAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAAATACAAAAAAATAGCTG
                                                                                                                                                                                                                                                                                                                                                                GCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTAGGTGGATCACCTGAGGTCAGAGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5670 BP;
                          GTCTCAAAAACAACAACAAAAAACAAAA 344
                                                                                     TGAACCCAGGAGGCAGAGGTTGCAGTGAGCACTCCAACCTGGGCAACAGAGTGAGACTCT
                                                                                                                                    AGATCGCAGAGTGAGCCGAAATCACAGATC----ACAGAGTGAGCAGAGTGAGACKCC 316
                                                                                                                                                                               GGCATGGTGGCAGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCT
                                                                                                                                                                                                                                                                                                                                                                                                           GCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATC
GTCTCAAAAAAAAAAAAAAAAAAAAAAA 5040
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7 2000US-023724P.
7 2000US-023729SP.
7 2000US-023729SP.
7 2000US-023742SP.
7 2000US-0237604P.
7 2000US-0237606P.
7 2000US-0237606P.
7 2000US-0244867P.
7 2000US-0245084P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 149.6;
Pred. No. 2.2e
1; Mismatches
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RESULT 34 ACA64883/c

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                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel reagent for diagnosis, molecular CC definition and therapy of chronic inflammatory joint diseases, and other CC inflammatory disorders, infective or tumour diseases in humans. The CC products of the invention have antiinflammatory, cytostatic, antirheumatic and immunosuppressive activity and can be CC used for gene therapy. The reagent of the invention and any proteins and CC used for medical diagnosis; (ii) for diagnosis and characterisation of CC chronic joint diseases, on the basis of molecular characterisation, and CC etermining the etiological pathogenicity principle of as yet cuncharacterised inflammatory diseases, also monitoring progression and/or CC treatment of disease, and optimisation of therapy and (iii) for CC treatment of disease, and optimisation of therapy and (iii) for CC treatment of disease, and optimisation of therapy and (iii) for CC treatment of disease, and optimisation of therapy and valuation of CC treatment of disease, and optimisation of therapy and valuation of the method of the invention
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                             Sequence 5670 BP; 1267 A; 1630 C; 1616 G; 1157 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page; 12pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reagents for diagnosis, study and therapy of chronic inflammatory joint and other diseases, comprises any of many specified genes or derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2001; 2001DE-01027572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chronic inflammatory joint disease; infection; tumour; antiinflammatory; cytostatic; antiarthritic; antirheumatic; immunosuppressive; gene therapy; etiological pathogenicity; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haeupl T,
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                                                                                                                                                                                 GAGACCATCCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTG
   TGAACCCAGGAGGCAGAGGTTGCAGTGAGCACTCCAACCTGGGCAACAGAGTGAGACTCT 5068
                                                                                                                                                AAGACCAGTCTGGCCAACATGGTGAAACCCCCGCCTCTACTAAAAATTACAAAAATTAGCTG
                                                                                                                                                                                                                   GCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTAGGTGGATCACCTGAGGTCAGAGGTTC
                                                                                                                                                                                                                                                      GCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATC
                                     AGATCGCAGAGTGAGCCGAAATCACAGATC-----ACAGAGTGAGCAGAGTGAGACKCC 316
                                                                        GGCATGGTGGCAGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCT
                                                                                                          GGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CD79a-B cell) DNA corresponding to U05259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprises
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            German.
                                                                                                                                                                                                                                                                                                         Score 149.6; DB 8
Pred. No. 2.2e-31;
                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                        60;
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                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                            5670;
                                                                                                                                                                                                                                                                                        6,
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ARESULT 35
ARE74508/C
ID AEF745
AC A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New kit comprising 10 and no more than 574 polynucleotides capable of specifically binding at least one specific polynucleotide sequence, useful for determining predisposition of a subject to develop PTSD, o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2006013561-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosis; gene regulation; gene expression; post traumatic stress disorder; psychiatric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2004; 2004US-0592408P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for diagnosing PTSD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID NO 22; 157pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorder; tranquilizer;
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The invention relates to a kit for determining predisposition of a cubject to developing post-traumatic stress disorder (PTSD) comprising at least 10 and no more than 574 polynucleotides, where each of the computation of a composition of the computation of the polynucleotides is capable of specifically binding at least one specific cited computising the polynucleotides cited, and a microarray computising the polynucleotides cited, and a microarray computising considered computation of the polynucleotides and a microarray computation of the coligonucleotides is capable of specifically binding at least one specific polynucleotide sequence. The kit computation of the polynucleotides selected from an oligonucleotide molecule, a cDNA molecule, a genomic considered from an oligonucleotide molecule, a cDNA molecule, a genomic considered from an oligonucleotide molecule, a cDNA molecule, a genomic considered from an oligonucleotide molecule, a cDNA molecule, a genomic considered from an oligonucleotide molecule, a cDNA molecule, a genomic considered for molecule and an NNA molecule. Each of the polynucleotides is at least one reagent constable for detecting hybridization of the polynucleotides and at least constable for detecting hybridization of the polynucleotides and at least considered for using the kit in determining predisposition of a packaging the kit in ferminate to developing PTSD. This sequence considered for the manufacture of a medicament identified for the polynucleotide of the invention. Note: The sequence considered for the polynucleotide of the polynucleotide sequence.
     Sequence 5670 BP;
                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                              for this patent did not form part of the printed specification, btained in electronic format directly from WIPO at
     1267
     A; 1630
C; 1616
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14-AUG-2000; 14-AUG-2000;

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Best Local Similarity
Matches 201; Conserv
                                                                                                                                                    11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; digestive system antigen; gene therapy; cancer; ulcerative colitis; infection; Hirschsprung's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human digestive system antigen genomic sequence SEQ ID
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07-JUL-2000;
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19-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCATGGTGGCAGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCT 5128
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                        2000US-0190076P.
2000US-0205515P.
2000US-0209467P.
2000US-0215135P.
2000US-0215135P.
2000US-021647P.
2000US-0217487P.
2000US-0217487P.
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2000US-0186350P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.4%;
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Pred. No. 2.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   appendicitis; chronic colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5670;
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                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention
                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders digestive system, particularly cancer and cancer metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
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                                                           TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAAATACAAAAAAATAGC
                                                                                                                  ATGCCTGTAATCCCAGCACTTTGGAAGGCCAAGGCGGGTGGATCACCTGAGGTCAGGAGT
                                                                                                                                                                                                                                                                             8205
    TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                           ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
                                        TCGAGACCAGCCTGGCAAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAATTAGC
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nilarity 75.5%;
Conservative
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2000US-0246610P.
2000US-0246611P.
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2000US-0249611P.
2000US-024920P.
2000US-0249211P.
2000US-024921P.
2000US-024921P.
2000US-024921P.
2000US-025921P.
2000US-025921P.
2000US-025921P.
2000US-0251868P.
2000US-0251989P.
2000US-0251989P.
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                                                                                                                                                                                              Score 149; DB 4; 1
Pred. No. 3.6e-31;
L; Mismatches 56;
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122-AUG-2000;
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26-SEP-2000;
27-SEP-2000;
28-SEP-2000;
29-SEP-2000;
20-OCT-2000;

2000US - 0225447P.
2000US - 022575PP.
2000US - 022575PP.
2000US - 022575PP.
2000US - 0226868P.
2000US - 022687PP.
2000US - 022687PP.
2000US - 022687PP.
2000US - 0229344P.
2000US - 0229344P.
2000US - 0229344P.
2000US - 023943PP.
2000US - 023943PP.
2000US - 0231243P.
2000US - 0231239P.
2000US - 024182P.
2000US - 024677P.
2000US - 024652P.
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antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
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06-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-2001
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25-SEP-2000;
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                                                                                 (HUMA-) HUMAN
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2000US-020551EP,
2000US-0216880P,
2000US-0216880P,
2000US-0225447P,
2000US-0231243P,
2000US-0231243P,
2000US-0231243P,
2000US-0231243P,
2000US-0231247P,
2000US-0231247P,
2000US-0246477P,
2000US-0246477P,
2000US-0246528P,
2000US-0246528P,
2000US-0249211P,
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                                                                                 GENOME SCI INC.
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The invention relates to novel genes (AAI62752-AAI62961) and proteins CC (AAM42347-AAM42415) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. CC The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and covarian cancer and other cancers of the adrenal gland, bone, bone marrow, concern the general gland, bone, bone marrow, consider the general gland, bone, bone marrow, consideration, autoimmune haemolytic consense, general, autoimmune haemolytic consultiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cc anaemia, autoimmune they colitis; (c) cc anaemia, autoimmune they colitis; (c) cc anaemia, autoimmune haemolytic consideration sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cc multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cc infections diseases e.g. cerebral anoxia and epilepsy; and (f) confections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly constructed the printed specification, but was obtained in electronic format directly constructed the printed specification, but was obtained pot sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel plasma membrane associated proteins useful for diagnosing, treating, preventing and/or prognosing disorders related to the including cancer, immune response and neuronal disorders.
Sequence 8205 BP; 2216 A; 1646 C; 1763 G; 2580 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-476225/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 276; 532pp + Sequence Listing; English
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밁 Ş 밁 Ś 맑 Ś B S 밁 S Matches Query Match Best Local 5420 5480 5540 5600 141 321 261 200; 81 Similarity ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA CAAGACTGC TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320 CGGGTGTGGTGGTGCGCCTATAATCCCCAGCTACTCAGGAGGCAGAGGTTGCAGTGAGC TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGGAGATTGCAGTGAGC TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC САЛАЛАСЛАСЛАСАЛАЛАЛСАЛАЛА 345 Conservative 37.3%; 75.5%; -GCCATTACACTCCGGCCTGGGCAACAAGAGCAAAACTCCATCT 1; Score 149; Pred. No. 3. Mismatches DB 4; .6e-31; 56; Length 8205; Indels 8 Gaps 5369 5421 140 5481 200 5541

RESULT 38

ADO79404 standard; DNA; 89900

26-AUG-2004 (first entry)

DPF3 region, SEQ ID 3.

Cytostatic; Gene therapy; breast cancer; human; DLG1; KIAA0783; DPF CENPC1; gene; ds; SNP; single nucleote polymorphism; D4, zinc and double PHD fingers, family 3; CERD4; cer-d4; FLJ14079; 2810403B03Rik; Rho family guanine-nucleotide exchange factor; chromosome 14q24.3-q31.1. Homo sapiens human; DLG1; KIAA0783; DPF3;

variation Location/Qualifiers

ξ

Barash

Ruben

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/standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a T/C SNP" 32003 /*tag= q /*tag= q /*standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a A/C SNP" 35588 /*tag= r /*standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a T/C SNP" 35619 /*tag= s	/note= "This SNP is described as a T/C SNP" 27402 /*tag= n /standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a A/G SNP" 28150 /*tag= o /standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a T/G SNP" 28494 /*tag= p	k If name= "Single nucleotide "This SNP is described as a I I name= "Single nucleotide "This SNP is described as a "This SNP is described as a "This SNP is described as a	/*tag= h /*tag= h /*tag= h /note= "This SNP is described as a G/C SNP" 18694 /*tag= i /*standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a A/G SNP" 18858 /*tag= j /*tag= j /*tag= j /standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a T/C SNP"	/standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a A/T SNP" 17179 /*tag= f /standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a C/G SNP" 18561 /*tag= g /standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a A/T SNP" 18658	/*tag= a /standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a A/C SNP" /*tag= b /standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a T/G SNP" 9719 /*tag= c /standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a A/G SNP" /*tag= d /standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a A/G SNP" 10481 /*tag= d /*tag= e /*tag= e	
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RESULT 39
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ID AREF926
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   Diagnosis; ss; gene; neurodegenerative disease; Alzheimers disease;
                                                             Human Ras effector protein Rin3, cDNA.
                                                                                                                                 20-APR-2006
                                                                                                                                                                                           AEF92655
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24-JUL-2003;
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72752
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                                                                                                                                 entry)
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his SNP is described as a T/A SNP"
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 149; DB 12;
Pred. No. 7.5e-31;
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P is described as a
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Matches

202; 84

Conservative

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Indels

1;

Gaps

143 82902

CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG

CCTGTAATGCCAGCACTTTGGAAGGCCGAGGTGGGAGGATCACCTGAGGTCAGGAGTCTG

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Concurodegenerative disease treatment, identifying a risk for a neurodegenerative disease in a test subject. Also included are diagnosing a neurodegenerative disease in a test subject. Also included are diagnosing concurred to a neurodegenerative disease in a subject, screening for a therapeutic concurred to a neurodegenerative disease in a subject, screening for a therapeutic concurred to a neurodegenerative disease treatment in a subject, identifying a risk concurred to a neurodegenerative disease treatment in a subject, identifying a risk concurred to a neurodegenerative disease in a test subject, identifying a risk concurred to a neurodegenerative disease in a test subject, identifying a risk concurred to a neurodegenerative disease in a test subject, a solid support comprising one or more biomarkers, where the biomarker is one or more comprising one or more biomarkers, where the biomarker is one or more concurred disease, ATP-synthase beta chain, concurred to the comprising protein and protein antigen, Prohibitin, Phosphoglycerate mutase 1, concurred transcripts comprising protein RAPIB, concurred transcripts comprising cyclin D1, cyclin B, cyclin G1, weel, hTR2, CDC25b, GSX3 beta, protein kinase c alpha, C5, C1 contichymotrypsin, HSP 27, HSP 90, crystalline, GAPDH, ferritin H, cordinative disease, screening a therapeutic agent for treating a neurodegenerative disease, monitoring a neurodegenerative disease concorression monitoring a response to a neurodegenerative disease
                Query Match
Best Local Similarity
                                                                                                                                   progression monitoring a response to a neurodegenerative disease treatment, identifying a risk for a neurodegenerative disease, and differentially diagnosing a neurodegenerative disease, e.g. Alzheimer's disease and Parkinson's disease, in a test subject. The present sequence is a CDNA for a human biomarker, used in a microarray in the method of the invention. NOTE: The specification describes AEF92574-AEF92813 (table
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease for diagnosing a neurodegenerative disease, screening a therapeutic agent for treating a neurodegenerative disease, monitoring neurodegenerative disease progression, monitoring a resname to neurodegenerative disease progression, monitoring a resname to neurodegenerative disease
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neuroprotective; nootropic; antiparkinsonian; screening; prog
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                                                                                                                    yet some are protein sequences
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                                                                            41095 C; 42605 G;
Score 149; DB 15;
Pred. No. 9.2e-31;
L; Mismatches 71;
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                                         DNA chip analysis as expression level to
                                                                                                                                                                                                                                                                                          Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
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       The invention relates to detecting (M1) granulocyte (GC) active (GCA), by detecting the level of expression of gene(s) (GS) ids (GCA), by detecting the level of expression of gene(s) comparing DNA chip analysis as given in the specification, and comparing expression level in an unactivated GC, very control of the control of GCA. Also included the control of the control of GCA included the control of GCA in the cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCG-GAGATTGCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGAGACCATCCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                          SEQ ID NO 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTARARARARARARARARARARARARARACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGCCTGGTGGCAGACGCCTGTAATCCCCAGCTACTCAAGAGTCGCTTGAACTCAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.3%;
nilarity 76.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weissman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glomerulonephritis; asthma; thrombosis;
                                                                                                                                                                                                                          114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chronic
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Pred. No. 1.1e-30;
1; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВÞ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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RESULT 42
ADA02774/c
ID ADA027
XX ADA027
XX O6-NOV
D7 06-NOV
XX XX
D8 Human
XX Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cd expression of at least one gene in Gs; (2) screening (M3) for an agent that alters the capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression (cd pathogen or sterile inflammatory disease using the gene expression and tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of cexpression in a sample of the tissue of gene (s) from Gs, where the level of expression in a sample of the tissue of gene (s) from Gs, where the level of expression in a subject, exposure of an allergic response in a subject to a pathogen or sterile conflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene (s) from Gs in the tissue. An if agent that modulates the expression of gene (s) from Gs in the tissue. M1 is useful for modulating GCA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation in a tissue, an allergic response in a subject, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult capsure of a subject to a pathogen or sterile inflammatory disease (e.g. cardiac reperfusion injury, renal reperfusion, protozoal infection, inflammation, and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially conditions. The present sequence represents a gene differentially capable of modulations of the above conditions of the printed specification, but was obtained in electronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Simi
Matches 229;
Human; carcinoma associated; oncogene; carcinoma; cancer; breast;
                                             Human ARHGEF1 carcinoma associated gene, SEQ ID NO:1292
                                                                                                06-NOV-2003 (first entry)
                                                                                                                                                   ADA02774
                                                                                                                                                                                           ADA02774 standard; DNA; 44075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 201143 BP; 50606 A; 49308 C; 49683 G; 51546 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCATGGTGGCACA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCATCCTGGC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACATTTTAACAATATTAATTCAGGCCAGGCATG----GTGGCTCATGCCTGTAATCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACCTGTAGTCCCAGCTACTCAGGA-----GCCGGAGATTGCAGTGAGCTGAGATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACTTTTGGAGGCTGAGACTGGCAGATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGGC
                                                                                                                                                                                                                                                                                                                                                                     CAACAAAAAACAAAAAAACCATAA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAACATGGTGAAACCCCCATCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTGGCAGG
                                                                                                                                                                                                                                                                                                                       AATTTGCTGÁGTÁATGÁACCÁAÁA 2910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAAAAACAA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCCTGGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAATATTAATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCTGTAATCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.16
1; Mismatches
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Pred. No. 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to recombinant carcinoma associated (CA) nucleic CC carcin sequences from mouse and human (AbA)1482-AbA03094), and to CC carcinobinant carcinoma associated proteins (CAP) encoded by them. The CC invention also encompasses expression vectors and host cells comprising a CC ch nucleic acid, a polypeptide (especially an antibody) that specifically compasses to the protein, and a biochip comprising CA nucleic acid or CC fragments thereof. The sequences of the invention were identified using CC oncogenic retroviruses, which insert into the genome of the host organism CC at random. Many of these do not carry transduced host oncogenes or CC pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host CC protooncogenes. The CA nucleic acid sequences can be used to diagnose CC carcinoma (especially breast cancer, prostate cancer, lymphoma or CC elukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular CC tissues. CA nucleic acids, proteins and antibodies are also useful as CC therapeutic agents and in screening and evaluating drug candidates. The CC present sequence represents a specifically claimed human CA nucleic acid Sequence of the invention. Note: The complete sequence data for this CC patent did not form part of the printed specification, but was obtained CC in electronic format directly from WIPO at CC fro, without into the sequences.
                                                                                                                                                                                                                                                                                                                                                                                  Matches 200;
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 44075 BP; 8314 A; 11402 C; 11137 G; 8371 T; 0 U; 4851 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 1292; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-587068/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-DEC-2001; 2001US-00035832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-DEC-2002; 2002WO-US041414.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                              8485
                                                                                                                               8545
                                                                                                                                                                                                                8605
                                                                                                                                                                                                                                                                                                 8665
                                                                                                                                                                      203
                                                                                                                                                                                                                                                       143 GAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTACTAAAAATACAAAAAATAGCTG
                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                             GGCATGGTGGCAGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCT 8486
                                                                                                                                                                    GGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTG
                                                                                                                                                                                                                                                                                                                                           GCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATC
    GTCTCAAAAACAACAACAAAAAAAACAAA 343
                                                                                                                                                                                                                AAGACCAGTCTGGCCAACATGGTGAAACCCCCGCCTCTACTAAAAATTACAAAAATTAGCTG
                                              TGAACCCAGGAGGCAGAGGTTGCAGTGAGCACTCCAACCTGGGCAACAGAGTGAGACTCT 8424
                                                                                     AGATCGCAGAGTGAGCCGAAATCACAGATC-----ACAGAGTGAGCAGAGTGAGACKCC 316
                                                                                                                                                                                                                                                                                                 GCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTAGGTGGATCACCTGAGGTCAGAGGTTC
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    37.2%;
                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 148.6; DB 9
Pred. No. 7.7e-31;
                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
                                                                                                                                                                                                                                                                                                                                                                                60;
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                                                                                                                                                                                                                                                                                                                                                                                                                            44075;
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                                                                                                                                                                                                                                                                                                   8606
                                                                                                                                                                                                                                                                                                                                           142
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RESULT 43
ADB72512/c
ID
ADB72512;
XX
ADB72512;
XX
ADB72512;
XX
OA-DEC-2003 (first entry)
XX
DE Human ARHGEF1 gene.
XX
Human i ds; cytostatic; gene ther
KW
cancer; neoplasm; adenocarcinoma
XX
WO2003008583-A2.
XX
PN
WO2003008583-A2.
XX
PD
SO-JAN-2003.
XX
PD
SO-JAN-2001; 2001WO-US051291.
XX
PD
SO-WAR-2001; 2001US-00094113.
PR
O2-MAR-2001; 2001US-00052482.
PR
O2-MAR-2001; 2001US-00052482.
PR
O3-NOV-2001; 2001US-000947722.
PR
O3-NOV-2001; 2001US-00034650.
XX
PD
WO203-239337/23.
XX
VX
PD
WO203-239337/23.
XX
New recombinant nucleic acid, usper cancers, neoplasm, adenocarcinom
XX
PT
Cancers, neoplasm, adenocarcinom
XX
CC. The invention relates to a novel cancinotide sequence selected from cactivity, and may have a under caccinom caccinomas, e.g. lymphomas, cancinomes, e.g. lymphomas, cancinomes, cancinomas, e.g. lymphomas, cancinomes, cancinomas, cancino
                                                                                     유 성 유 성
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rocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a human gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 340; 2304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancers, neoplasm, adenocarcinoma, or sarcomas.
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neoplasm; adenocarcinoma; sarcoma; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 148.6; DB 10;
Pred. No. 7.7e-31;
1; Mismatches 60;
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  8399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a recombinant nucleic acid comprising a nucleotide sequence selected from any of the fully defined carcinoma-associated (CA) genes from the 50 tables given in the specification. The CA proteins are secreted, transmembrane or intracellular proteins. The recombinant nucleic acids are useful for screening for drug candidates for diagnosing or treating carcinomas. Sequences given in ADC85215-ADC85514 represent CA genes of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant nucleic acid comprising a nucleotide sequence the carcinoma-associated (CA) genes, useful for screening for candidates for diagnosing or treating carcinomas.
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                                                                                                     TGAACCCAGGAGGCAGAGGTTGCAGTGAGCACTCCAACCTGGGCAACAGAGTGAGACTCT
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Pred. No. 7.7e-31;
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RESULT 45 ADM74369/c

ADM74369 standard; DNA; 44075 BP

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cy method of diagnosing carcinoma comprises determining the expression of cy one or more genes comprising the nucleic acid sequence in a first tissue type of a first individual and comparing the expression of the gene from type of a first individual and comparing the expression of the gene from cy unaffected individual, where a difference in the expression indicates chat the first individual or a second cy unaffected individual, where a difference in the expression indicates chat the first individual has carcinoma. A method of inhibitor to the CAP. Treating carcinomas comprises administering to a patient an inhibitor of CAP. Comprises binding an inhibitor to the CAP. Treating carcinomas comprises administering to a patient an inhibitor of CAP.

CC Neutralising the effect of a CAP comprises contacting an agent specific cy for the CAP. The polypeptide specifically binds to the protein encoded by the nucleic acid. It comprises an antibody that specifically binds to the protein encoded by the nucleic acid. The nucleic acids are useful for cy preparing a composition for diagnosing or treating carcinoma e.g., cy leukaemia or lymphoma. This sequence represents a human carcinoma e.g., cy leukaemia or lymphoma. This sequence represents a human carcinoma conditions and conditions are useful for this patent did not form part of the printed specification but was cobtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to new recombinant nucleic acids. The invention CC also relates to a host cell comprising a recombinant nucleic acid or cexpression vector, an expression vector comprising a recombinant nucleic cc acid, a recombinant protein, a method of screening for drug candidates, a CC method of screening for a bioactive agent capable of binding to a carcinoma associated protein (CAP) encoded by a nucleotide sequence, a cc method of screening for a bioactive agent capable of modulating the carcinoma drug, a method of evaluating the effect of a candidate cd carcinoma drug, a method of dagnosing carcinoma, a method of carcinoma, a method of neutralising the effect of a CAP and a method of diagnosing carcinoma or comprises defect of a patient, removing a call sample from the patient and determining alterations in the expression or activation of a gare comprises derivation of a sequence. A method of diagnosing the nucleotide sequence. A method of diagnosing the patient and determining alterations in the condition of a gare comprises derivation of a garence. A method of diagnosing the nucleotide sequence. A method of diagnosing carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New carcinoma associated gene or protein, useful for preparing a composition for diagnosing or treating carcinoma e.g., leukemia or
                                           seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 40;
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02-MAR-2001; 2001US-00798586.
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Query Match

37.2%;

Score 148.6;

DB 12;

Length 44075

Sequence 49745 BP; 10151 A; 14745 C; 14496 G; 10151 T; 0 U; 202 Other;

Sequence 44075 BP; 8314 A; 11402 C; 11137 G; 8371 T; 0 U; 4851 Other,

RESULT 46 ACN45134 S 밁 Ś 밁 Ś 뮍 Ś 멼 Matches Best Local Similarity are associated with carcinomas. The sequences are useful for: (1) for screening drug candidates; (11) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (111) for screening of a bioactive agent capable of modulating the activity of CAP; (1v) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (1x) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for WPI; 2003-328604/31 Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence. 01-MAR-2002; 2002US-00087192 28-FEB-2003; 2003WO-US006235 WO2003073826-A2 Cytostatic; Human genomic sequence hCG31443. 18-NOV-2004 ACN45134; ACN45134 standard; DNA; 49745 Homo sapiens (SAGR-) SAGRES DISCOVERY. 8485 8545 8425 GTCTCAAAAAAAAAAAAAAAAAAAAAA 8399 8605 8665 317 263 203 143 GAGACCATCCTGGCCAACATGGTGAAAACCCCGTCTTTACTAAAAAATACAAAAAATAGCTG 83 GCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATC SEQ TGAACCCAGGAGGCAGAGGTTGCAGTGAGCACTCCAACCTGGGCAACAGAGTGAGACTCT 8426 AAGACCAGTCTGGCCAACATGGTGAAACCCCCGCCTCTACTAAAAATACAAAATTAGCTG GCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTAGGTGGATCACCTGAGGTCAGAGGTTC GTCTCAAAAACAACAACAAAAAAAACAAA AGATCGCAGAGTGAGCCGAAATCACAGATC-----ACAGAGTGAGCAGAGTGAGACKCC GGCATGGTGGCAGGCGCCTGTAATCCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCT GGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTG carcinoma; lymphoma; cancer; Conservative ID NO 1930; Opp; English. (first entry 74.9%; 1. Pred. No. 7.7e-31; ВÞ 343 human; gene; Indels ٠ ر Gaps 8486 8606 8546 142 262 202

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RESULT 47
AEE04996 2
Continuation (3 of 5) of
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WP Sequence split into 5
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Matches 206
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Best Local Similarity
Matches 219; Conserv
Human; p53 pathway; phosphatidylinositol biphosphate; PIB; therapeutic;
                          Human phosphatidylinositol biphosphate (PIB) DNA #1.
                                                          26-JUN-2003
                                                                                      AAD54538;
                                                                                                                 AAD54538
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                                                                                                               standard;
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Begin End
                                                          entry)
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Pred. No. 8e-31;
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RESULT 49 ADH76849 ID ADH76 XX

ADH76849

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                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method of identifying candidate p53 pathway-modulating agents. The method involves screening for agents that modulate the activity of phosphatidylinositol biphosphate (PIB). The methods are useful for identifying candidate p53 pathway-modulating agents used as therapeutic targets for disorders associated with defective p53 function. They are also useful for modulating p53 pathway in a mammalian cell or for diagnosing or treating a disease associated with defective p53 function, e.g. cancers such as breast cancer, colon cancer, lung cancer or ovarian cancer. Sequences of the invention are useful for in vivo assays to test the activity of candidate p53-modulating agents or to assays to test the activity of pathway process such as apoptosis or cell proliferation. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-2001; 2001US-0296076P
10-OCT-2001; 2001US-0328605P
15-FEB-2002; 2002US-0357253P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying candidate p53 pathway-modulating agents, useful as therapeutic targets for disorders associated with defective p53 f comprises screening for agents that modulate phosphatidylinositol biphosphate activity.
                                                                                                                                                                                                                                                                                                                                                                             Sequence 133893 BP; 33343 A;
                                                                                                                                                                                                                                                                                                                                                                                                            sequence is human PIB DNA
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                                                            CTTAAACCTGGGAGGTGGAGGTTGTACCAAGCGGAGATCGTGGAGACAGAGCAGGCCCCCT
                                                                                                                                                                                       TTGAAACCAGCCTGGCCAACATGGTGAAAACCTCATCTCTACTAAAAAATACAAAAATTAGC 127504
                                                                                                                                                                                                           TCGAGACCATCCTGGCCAACATGGTGAAAACCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                     ACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCAGGCGGATCACCTGAGGTCTGGAGT 127444
                                                                                                                                                                                                                                                                                 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                              TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
GTCTCAAAAAACAAAACAAAACAAAACCCCCAAAAAA
                               CAAAAACAACAAAAAAAACAAAAAACCATAAGACA
                                                                                           TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGGAGTGAGACKCCGTCT 320
                                                                                                                            TGGGTGTGGTGGCACACCTGTAGTCGCAGCTACTCCGGAGGCTGAGGCAGGAGAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 39-111; 139pp;
                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 1.1e-30;
1; Mismatches 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single nucleotide polymorphism; anorectic; gene therapy; obesity; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             melanin-concentrating hormone receptor 1; MCHR1; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Melanin-concentrating
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                                                                   /standard name= "Single nucleotide polymorphism"
replace(103270,A)
                                                                                                                                                                                                                                                                                                                                                                                                                             /standard_name= "Single nucleotide polymorphism"
replace(96227,A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /standard_name= "Single nucleotide polymorphism"
replace(95767,C)
                                                                                                   /standard_name= "Single replace(103156,C)
                                                                                                                                                                                                   /standard_name= "Single nucleotide polymorphism"
replace(99803,G)
                                                                                                                                                                                                                                                                                                 /standard_name= "Single nucleotide polymorphism"
replace(98848,T)
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replace(97004,G)
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replace(96797,A)
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replace(95538,G)
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replace(101352,T)
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replace(97723,T)
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                                                                                                                                                                    /standard_name= "Single nucleotide polymorphism"
ceplace(100220,A)
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eplace(99450,A)
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eplace(99142,A)
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18-DEC-2003

RESULT 50 AAK79514 ID AAK79

AAK79514 standard;

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Best Local Similarity 67.8
Matches 221; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence comprising one or more of the nucleotide exchanges (SNP's) given in the specification and at least 8 bases of surrounding sequence of the MCHR1 gene. The composition has anorectic activity. The polynucleotide composition may be used in gene therapy to treat the disorders of the invention. The composition is useful for disgnosing obesity related to the presence of a molecular variant of the MCHR1 gene or a susceptibility to the disorder. The MCHR1 protein or polynucleotide is useful for preparing a medicament for treating or preventing obesity related to the presence of a molecular variant of the MCHR1 gene. This polynucleotide prepared to the invention. This sequence is not shown in the specification. It has been taken from the GenBank accession number Z86090 provided in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel diagnostic polynucleotide composit The polynucleotide composition comprises: a sequence encoding a polypeptide with defined sequences given in the specification; a secapable of hybridizing to a melanin-concentrating hormone receptor (MCHR1) gene; a polynucleotide encoding an MCHR1 polypeptide; or a melanin-concentration polypeptide; or a melanin-concentration of the metallication of the metall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 122557 BP; 34723 A; 28259 C; 27523 G; 32052 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New diagnostic composition, useful presence of a molecular variant of the disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-062377/06.
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                                                      АЛАЛАСААСААЛАЛААСААЛАЛА 347
                                                                                                                   GAACCCGGGAGGCAGAGGTTGCAGTGGGCCGAGATCGTGCCAAGAGTGAAACTCCCTCTC
                                                                                                                                                                                                                                         GCATGGTGGCAGGCACCTGTAATCCCAGCTACTTGGGAGGGCTGAGGCTGGAGAATTGCTT
                                                                                                                                                                                                                                                                                                                                                                  AGACCAGACTGGCCAACATGGTGAAAACCCCCGTCTCTACTAAAAATACAAAAATTAGCCAG
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AAAAAAAAAAAAAGAAAGAAAGAAAA 68308
                                                                                                                                                                         GATCGCAGAGTGAGCCGAAATCACAGATCACAGA--GTGAGCAGAGTGAGACKCCGTCTC
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Séarch completed: July 17, 2006, 20:16:38
Job time : 542 secs
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AF305828 Homo sapi
DA307259 DA307259
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sapiens genomic clone RPCI-11-153H2,
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AA642809 nu05a06.s
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AQ380981 RPCI11-16
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B85944 RPCI11-2111
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BU527958 AGENCOURT
AA654778 nt73g01.s
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Other GSSs: RPCII1-153H2.TV

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Email: hbe@tigr.org

Clones are derived from the human BAC library RFCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet cs (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: SP6

Class: BAC ends.
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ACPT APCI-11-Seg1-4-200N9-T7 RPCI-11 Human segment 1-4 genomic library Homo sapiens genomic clone RPCI-11-Seg1-4-200N9-T7 similar to Human AQ936397.1 GI:6654471

GSS.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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BAC End Sequences
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/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site 1:
RPCII1 Human Male BAC Library"
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/mol_type="genomic DNA"
/db_xref="GDB:7558537"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
                                                                                                                   617 bp
0j49905.yl Human lacrimal gland,
clone 0j49905 5', mRNA sequence.
CK430465
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: pdejong@mail.cho.org
BAC end sequences. For clone availability please contact
Jong (pdejong@.mail.cho.org). BACPAC Resources WWW site:
www.chori.org/bacpac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: de Jong, P.J.
Children's Hospital Oakland Research
747 Fifty second Street, Oakland, CA
Tel: 510 450 7911
Fax: 510 450 7924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Osoegawa,K., Mammoser,A.G., Wu,C., Frengen,E., Zeng,C., Catanese,J.J. and de Jong,P.J.
A bacterial artificial chromosome library for sequencin complete human genome
                                                   Homo sapiens
                                                                                               CK430465.1 GI:40678584
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                                                                Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                            TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGA-----GCCGGAGATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="Lymphocyte"
/clone_lib="RPCI-11 Human segment 1-4 genomic library"
/note="Vector: pBACe3.6; BAC clones in E. coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="RPCI-11-Seg1-4-200N9-T7"
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4e-19;
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unamplified: oj Homo sapiens cDNA
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AUTHORS
                                                                                   DEFINITION
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801 k
AGENCOURT 10405312 NIH MGC_82
5', mRNA sequence.
BU568469
BU568469.1 GI:22918758
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Ozyildirim,A.M., Wistow,G.J., Gao,J., Wang,J., Dickinson,D.P., Prierson,H.P. Jr and Laurie,G.W.
The lacrimal gland transcriptome is an unusually rich source of rare and poorly characterized gene transcripts
Invest. Ophthalmol. Vis. Sci. 46 (5), 1572-1580 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: graeme@helix.nih.gov
Plate: 49 row: g column: 0
Seg primer: M13RP1 reverse p
Location/Qualifiers
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Fax: 301 496 0078
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National Eye Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="Human lacrimal gland, unamplified: oj"
/note="Organ: Eye; Vector: pCMVSport6; RNA was extracted
from 2 human lacrimal glands. A directionally cloned cDNA
library in the pCMVSpORT6 vector(Life Technologies) was
constructed at Bioserve Biotechnology (Laurel MD)
essentially following the protocols of the SuperScript
Plasmid System full details of which are contained in the
manufacturer's Instruction manual
(http://www.lifetech.com/). First strand synthesis was
carried out using a Not I primer-adapter
[5'-pGACTAGTTCTAGATCGGACCGCCCC(T)15-3']. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="lacrimal gland"
/dev_stage="Adult"
/lab_host="EMDH10B"
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'db_xref="taxon:9606"
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Geisel,G., Jo M., Martin,J.,

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AA405549/c
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                   sequence.
                                                         AA405549 357 bp mRNA zw39f03.rl Soares total fetus Nb2HF8 9w IMAGE:772445 5' similar to contains Alu
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
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AA405549.1
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                                                                                                                                                                                                                                                                                     GCTCGCA-----CCATTGCACTCCAGCCTGGGTGAAGAGCGAGACTCTATCTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clones and was constructed by Clontech Alto, CA)."
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:6615547"
/lab_host="DH10B (T1_phage-resistant)"
/clone_lib="NIH_MGC_82"
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                                                             Homo sapiens cDNA clone repetitive element;, mRI
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BE149224 40
RC2-HT0552-120200-014-c06 H
BE149224 BE149224.1 GI:8611948
EST.
Homo sapiens (human)
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Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-Merck EST project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                               GCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAGATCGCA 270
                                                                                                                                                                                                                                                                                                                     CTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                 CCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCATC
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                                                                                                                                                                                                             GCATGCACCTGTAATCCCGGCTACTCGGGAGGCTGAGGTTGCAGTGAGCCAAGATTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATCCGGAGATAAAGAAATTGAGGCATGAATTGGCTGGGCACGGTCGTCACGCCTGTAAT 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
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/mol_type="mRNA"
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lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 151; DB 1
Pred. No. 5e-19;
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC2-HT0252-120
200-014-c06&t3=2000-02-12&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence tags
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                                                                   AAAACAAACAAACAAAAAAACAGA 303
                                                                                                АВАВСКАСВАСВАВАВАСВАВАВ 345
                                                                                                                                    AGATCGCACTACTGCACTGCACTCCAGCCTGGGTGA - CAGAGCAAGACACTGTCTCA
                                                                                                                                                                    AGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCA
                                                                                                                                                                                                     GGCGTGGTGGCACCTGTAATCCCAGCTACTCAGGAGGCAGAGGTTGCAGTGAGCCA
                                                                                                                                                                                                                            GGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGACCCGGAGATTGCAGTGAGCTG
                                                                                                                                                                                                                                                                        AGACCAGCCTGGCCAACATGTGTAAAACCCCCGTCTCTACTAAAAATACAAAATTAGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=Torgan: head neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo gapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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                                                             CZ455807 613 bp DNA MCF738H04TF Human MCF7 breast cancer cel Homo sapiens genomic clone MCF7_38_H04,
Homo sapiens (human)
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Query Match
Best Local S
Matches 197
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197; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.

Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
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Regenerative Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: rbrandenberger@geron.com
Insert Length: 513 Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 Constitution Drive, Menlo Park, CA 94025, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Geron Corporation
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                 TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC
AAAAACAAAACAAACAAACAAACAAAAAAAAACAAC 326
                                        CAMAMACAACAACAAAAAAAAAAAAAAACCATAAGAC 356
                                                                                     TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                                                                       TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                       TTGAGACCAGCCTGGCCAACATGATGAAACCCCCGCCTCTATTAAGAGTACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                 ATGCCTGTAATCCTGGCACTTTGGGAGGCCAAGGCGTGTGGATCATTTGCGGTCAGGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="CRN_PREHEP"
/noce="oligo dT primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="embryonic stem cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 149.6; DB 8 Pred. No. 8.6e-19; D; Mismatches 79
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sapiens cDNA 5', mRNA sequence.
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GI:77932102

NA linear GSS cell line library 04, genomic survey

GSS 20-OCT-2005

(MCF7

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REFERENCE
AUTHORS
                                                  ACCESSION
VERSION
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ORGANISM
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DB313291/c
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                                                                                                   DEFINITION
                                 KEYWORDS
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Best Local S
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                                                 sequence.
DB313291
DB313291.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 613)
Volik,S.V., Raphael,B.J., Huang,G.-Q., Murnane,J., Brebner,J.H.,
Volik,S.V., Raphael,B.J., Tao,Q., Kowbel,D., Lapuk,A.V., Kuo,W.-L.,
Bajsarowicz,K., Paris,P., Tao,Q., Kowbel,D., Lapuk,A.V., Kuo,W.-L.,
Shagin,D.A., Shagina,I.A., Magrane,G., Gray,J.W., Jan,F.-C., de
Jong,P., Pevzner,P. and Collins,C.
Decoding the genomic architecture and high throughput detection of
fusion transcripts in breast cancer cell lines: implications for a
                 Homo
                                   EST.
                                                                                                  Class: BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: svolik@cc.ucsf.edu
This clone is available from Amplicon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.genomex.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Volik SV
Colin Collins' lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                CAAAAACAACAACAAAAAACAAAAAA 346
                                                                                                                                                                                                                                                                                                        TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                                        CCÁGATCACGCCACTGCACTCCACCCTGGGTGA-
                                                                                                                                                                                                                                                                                                                                                              TGGGCATGGTGGCACACACCTGTAGTCCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
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                                                                                                                                                                                                       CAAAAAAAAAGAAAAGAAAAGAAAA 343
                                                                                                                                                                                                                                                                                                                                         TGGACATGCTGGCAGACGCCTGTAGTCCCCAGCTCCCCTGGAGGTTGGAGCTTGCAGTGAGC
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Box 0808, San Francisco,
415 502 7066
415 502 5665
sapiens (human) sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/clone="MCF7_38_H04"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pECBAC1; Site_1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 procedure."
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                                                    GI:83195301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cancer Center
Francisco, CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 149.6; DB 13; Pred. No. 8.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                     cDNA clone CTONG2000516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94143-0808, USA
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RESULT 10
AQ541320/c
                                              SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   506
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1 (bases 1 to 542)

1 (bases 1 to 542)

1 (bases 1 to 542)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Yamashita, R., Yamamoto, Y., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishidas, S., Ishibashi, T., Takahashi-Fujii, A., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification and Characterization of Putative Alternative Promoters of Human Genes
                                                                                                                                                    AQ541320
RPCI-11-343C15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-343C15, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                 SSD
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2-6-7 Kazusa-Kamatari, Kisarazu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLJ Project (HRI Team)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16344560
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                                           Homo sapiens
                                                                                                                  AQ541320.1 GI:4871776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 81-438-52-398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 81-438-52-3975
                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCTGTAATCCCAGCACTTTGGNAGGCCAAGGCTGGCAGATCACTTGAGGTCAGGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATC 142
                                                                                                                                                                                                                                                                                                                               AGATTGCGCCACTGCACTCCAGCCTGGGCGACACAGTGAG
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CTONG2000516"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="tongue, tumor tissue"
clone_lib="CTONG2"
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Pred. No. 1.3e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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RESULT 11
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Zhao, S.,
Venter, J.
Use of BA
                                                                                                                    sequence.
DA572262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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DA572262 HEMBB1
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EST.
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Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shaying Zhao, William Nierman, Department of Bukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other_GSSs: RPCI-11-343C15.TJ
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                                                                Homo sapiens (human)
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of BAC End Sequences from Library RPCI-11 for Sequence-Ready
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Adams,M.D., Nierman,W., Malek,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7631390"
/db_xref="taxon:9606"
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72.1%;
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Pred. No. 1.4e-18;
1; Mismatches 72
                                                                                                                                                      cDNA
                                                                                                                                                      mRNA
clone
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                                                                               sequence.
AG170656
AG170656.1
GSS.
 Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes Genome Res. 16 (1), 55-65 (2006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: flj-cdna@nifty.com
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute (HRI); cDNA library construction: Department
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                      Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo
                                                              Pan troglodytes (chimpanzee)
                                                                                                                                                                         AG170656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16344560
                                                                                                                                                                                                                                                                                              AAACAACAACAAAA 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="HEMBB1"
/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="whole embryo, mainly body"
/dev_stage="embryo, 10 weeks"
/clone_lib="HEMBB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMBB1000862"
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                                                                                                   GI:16700334
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Pred. No. 1.3e-18;
1; Mismatches 52
                                                                                                                                                        clone:
                                                                                                                                                                         691
                                                                                                                                                    1 bp DNA
RP43-039L04.TJ,
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Gaps

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09-JAN-2002

297 323 263

411 203 471

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                          602277287F2 NIH_MGC_86 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
Hominidae; Homo
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                              Homo sapiens
                                                              Homo sapiens (human)
                                                                                 EST
                                                                                               BF965924.1 GI:12333139
                                                                                                                BF965924
                                                                                                                              mRNA sequence.
                                                                                                                                                                 BF965924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Totoki,Y., Watanabe,H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fujiyama, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing: TJ
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                                                                                                                                                                                                                                                                      CACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAAAAAACAACAACAACAAAAAAAACAA 342
                                                                                                                                                                                                                                                                                                                                        GTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAAT
                                                                                                                                                                                                                                                                                                                                                                                     TGAAACCCTGTCTCTACAAAAAATACAAAACTTAGCTGGACATGGTGGCATGCACCTGTA
                                                                                                                                                                                                                                                                                                                                                                                                      TGAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCATGGTGGCACACACCCTGTA
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                                                                                                                                                                                                                                                   CCTGGGCCA-----
                                                                                                                                                                                                                                                                                                                   GTCCCAGCTACTCAGGAGGCTGAGATTGCAGCGAGCCAAGATTGCACCATTGCACTCCAG
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R.Site 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'cell_type="lymphocytes"
'clone_lib="RPCI-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="RP43-039L04.TJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mol_type="genomic DN
db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Pan troglodytes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.0%;
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: EcoRI
: EcoRI.
                                                                                                                                                                                                                                                   Score 148; DB 14;
Pred. No. 1.7e-18;
1; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ., Toyoda, A., and Sakaki, Y.
                                                                                                                                                               749 bp
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                                                                                                                                                sapiens
                                                                                                                                                                 mRNA
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                                                                                                                                                cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 691;
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                                                                                                                                                               linear
                                                                                                                                                 IMAGE: 4365117
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REFERENCE
AUTHORS
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AQ341973
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           Hominidae; Homo.

1 (bases 1 to 538)
Zhao,S., Adams,M.D., Nierman,W., Malek,J.,
Venter,J.C.
                                                                                                                                                                                                    AQ341973
RPCI11-111D18.TV RPCI-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, 1
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                     AQ341973
AQ341973.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM10013 row: m column: 22
                                                                                                           Homo sapiens
                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                    genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGCGTGGTGGCGCACATCTGTAGTCCCAGCTACTCGGGAG--GCTGAAGCACGAGAAT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGAGACCATCCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAAATACAAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                             CAAAAACAACAACAAAAAACAAAAAAAC 348
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                                                                                                                                                                                                                                                                                                CAAAAAAAAAAAAACAGAAGAAAGAAAC
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                                                                                                                                                                                                                                                                                                                                                                                         TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGCAGATCACCTGAGGTTAGGAGT 196
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Location/Qualifiers
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                                                                                                                                                        GI:4166869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.0%;
                                                                          Chordata; Craniata; Vertebra
Euarchontoglires; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 148; DB 2; Length 749; Pred. No. 1.6e-18; Mismatches 66; Indels
from
                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                    538 bp
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Library RPCI-11 for Sequence-Ready
                                                                                                                                                                                                     sapiens
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                                                                                         Vertebrata; Euteleostomi;
                             de Jong, P. and
                                                                                                                                                                                                                  linear
                                                                            Catarrhini,
                                                                                                                                                                                                     GSS 06-MAY-1999
RPCI-11-111D18,
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                                                                                                                                                                                                                                                                                                                                                                                342 TGAGCCTGAGATCGTGCCACTGCACTCCAGCTTGGGCAACAGAGTGAGACTCTGTCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 GCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGA
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                                                                                                                                                                                                                                                                                                                   402
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                                                                                                                                                                                                                                                                                                                                                                                                               264 GATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGAGTGAGACKCCGTCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                repetitive element ;, 1
AA648957
AA648957.1 GI:2575386
                                                                                                                                                                                                AA648957

ABCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1185176

Similar to contains Alu repetitive element;contains element PT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jope
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or fi
Research Genetics (info@resgen.com). BAC end search page:
1 (bases 1 to 426)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                      EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Shaying Zhao, William Niern
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                  Hominidae; Homo.
                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Map Building
                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGACCATCCTGGCCAACATGGTGAAAACCCCGTCTTTACTAAAAAATACAAAAAATAGCTGG
                                                                                                                                                                                                                                                                                                                   ATAATAATAATAATAGTAATA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCATGGTGGCACGCACCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAG-GATCACT
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/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1:
RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/db_xref="GDB:7542329"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RPCI-11-111D18"
/sex="Male"
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                                                                                                                                                                                element ;, mRNA sequence.
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Pred. No. 2.1e
1; Mismatches
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   Hominidae; Homo.
1 (bases 1 to 897)
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Local Similarity
nes 224; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  219 TGCCTGTAATCCCAGCTTCTCGGGAGGCTGAGGTAGGAGAATCACTTGAACCCAGAAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 AAATATTAATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCTGTAATCCCAG
                                                                     DR759556
DR759556.1
EST.
                                                                                                                   DR759556
HESC4_105_B07.g1_A037 NIH_MGC_262
IMAGE:7968807 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
unknown library type
Seq primer: -40ml3 fwd. ET f
                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
Contact: Robert Strausberg, Ph.D
                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                            AAAAAAAAAAAAAA 85
                                                                                                                                                                                                                                                                                                              GGAGGTTGCAGTGAGCCGAGATCAACCTGGGAGACAGAATGAGACTCCATCTCAAAAAAA
                                                                                                                                                                                                                                                                                                                                    AGAGTGAGCCGAAAATCACAGAGTGAG-CAGAGTGAGACKCCGTCTCAAAAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="germinal center B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="IMAGE:1185176"
                                                                                       GI:71052256
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71.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 147.4; DB 1
Pred. No. 2.4e-18;
L; Mismatches 82
                                                                                                                                         Нопо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                         mRNA
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                                                                                                                                       sapiens
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RESULT 17
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TOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                       653
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                                                                                                                                    773
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High quality sequence stop: 897.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Express Genomics, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
University of Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM 17081 row: c column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: BresaGen, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Emaıl:
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                                                                                                                                                                                                                                                                                                                             TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                        ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                    CAAAAAGAAAAGAAAAAA 848
                                                                                          CAAAAACAACAACAAAAAAA 340
                                                                                                                                  CTTGAACCCAGAAGGTGAAGGGCACAGTGACC---
                                                                                                                                                                      TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                                                             TGGGTATGGTGCATGCCTGTAATCCCAGCTACTAGGGAGGCTGAGGCAGGAGAATCA
                                                                                                                                                                                                                                                   TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                                       TCGAGACCAGCCTGGCCAACATGGTGAAACTCCATCTCTACTAAAAATACAGAAATTAGC
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primer: JENREV (CAGGAAACAGCTATGACC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pExpress-1; Site 1: NotI; Site 2: EcoRV;
/note="Vector: pExpress-1; Site 1: NotI; Site 2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos and
differentiated to an early neural progenitor cell type.
Cell line id and NIH Registry designation is BGO1.
Positive for Nestin and Musashi expression. Passage number
18. CDNA primed using oligo-dT primer:
18. CDNA primed using oligo-dT primer:
19. CDNA primed using oligo-dT primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Frederick, MD). Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. this is a Mammalian Gene Collection library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the EcoRV/NotI sites of pExpress-1. This primary library is non-normalized (normalized primary library is NIH_MGC_259). It was constructed by Express Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="human embryonic stem cells"
/cell_line="BG01"
/cell_line="BG01"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="NIH_MGC_262"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="embryonic stem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="IMAGE:7968807"
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db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 147.2; DB 10;
Pred. No. 2.2e-18;
1; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                    - AGGCGCCAGAGTGAGACTCTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    897;
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DA500385/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   141 TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAAATAGC
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DA500385.1
EST.
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DA500385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end of pass sequencing: RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.

(bases 1 to 486)

(bases 1 to 486)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Yamashita, R., Yamamoto, J., Sekine, M., Tsunitani, K., Kushida, N., Yamashita, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yonoyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M. Murakawa, K., Ishida, S., Ishidashi, T., Takahashi-Fujii, A., Murakawa, K., Ishida, S., Ishidashi, T., Takahashi-Fujii, A., Sigano, S., Saito, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification and Characterization of Putative Alternative Identification and Characterization of Putative Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                               САЛАЛАСЛАСЛАСАЛАЛАЛСЛАЛАЛАЛ
TAAATAAATAAATAAAATAAAATACA
                                                                                                                                                       TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                                                                                                            TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                                                                                                                                                                                                                               ACGCCTATAATCCCAGCACTTTGGGAGGCTGAGGCCGGTGGATCACCTGAGGTCAGGAGT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                    TCAAGACCAGCCTGGCCAACACAGTGAAACCCCCATCTCTACTAAAAATACAAAAATTAGC
                                                                                                                                                                                                            TGGGCATGATGGTGCATGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGTTGCAGTGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="brain"
/dev_stage="fetal"
/clone_lib="FCBBF3"
/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:9606"
clone="FCBBF3014320"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 147; DB 9;
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MEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
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Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bequence.
DA180817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16344560
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DA180817 BRAMY2 Homo sapiens cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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                                                           CAAAAACAACAACAAAAAACAAAAAAA 347
                                                                                                                                                                                                                                                                                                                                                                                                   TCAAGACCAGCCTGGCCAACACAGTGAAAACCCCATCTCTACTAAAAATACAAAAATTAGC
                                                                                                                              CAAGATCGCACAACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCGTCTCCCAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRAMY2045648"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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clone_lib="BRAMY2"
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG258140 545 bp mRNA linear EST 13-FEB-2001 602379239F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4510256 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plate: LLAM10391 row: m column: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                    CAAAAACAACAACAAAAAAACAAAAAAA 347
                                                                                CAAGATCGCACAACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCGTCTCCCAAAAAA 206
                                                                                                                       TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
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TAAATAAATAAATAAATAAAATACA 179
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                                                                                                                                                                                                      TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
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                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="embryonal carcinoma, cell line"
/lab host="PH10B (phage-resistant)"
/clome libe"NIH_MGC 92"
/clome libe"NIH_MGC 92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size_2.5 bb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4510256"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 147; DB 2;
Pred. No. 2.7e-18;
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RESULT 20 DA158439/c

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AUTHORS
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Best Local Similarity
Matches 192; Conserv
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                                                                                                                                                                                                                                                                                                                                                        372
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132
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                                                                                                                                                                                                                                                                                                          141 TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                  81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae; Homo.

1 (bases 1 to 547)

1 (bases 1 to 547)

Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S. Diversification of Transcriptional Modulation: Large-scale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DA158439 BRAMY2 Homo sapiens cDNA clone
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Helix Research Institute
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Genome Res. 16 (1), 55-65 (2006)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16344560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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TAAATAAATAAATAAATAAAATACA 106
                                                                                                                       TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCCAGAGTGAGACKCCGTCT
                                         CAAAAACAACAACAAAAAACAAAAAA 347
                                                                                       CAAGATCGCACAACTGCACTCCAGCCTGGGTGACAGAGCAAGAGCTCCGTCTCCCAAAAAA 133
                                                                                                                                                                            TGGGCATGATGCTGCATGCCTAATCCCAGCTACTTGGGAGGCTGAGGTTGCAGTGAGC
                                                                                                                                                                                                                   TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                 TCAAGACCAGCCTGGCCAACACAGTGAAACCCCATCTCTACTAAAAAATACAAAAATTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="amygdala"
/clone lib="BRAMY2"
/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRAMY2017998"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 147; DB 9;
Pred. No. 2.7e-18;
0; Mismatches 75
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BRAMY2017998 5', mRNA
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RESULT 21

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REFERENCE
AUTHORS
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Best Local
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DB176347
DB176347.1
EST.
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DB176347
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Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,

Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,

Yanishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,

Ishii, S., Sugiyama, T., Saito, K., Yokoi, T., Kondo, H., Wagatsuma, M.

Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.

Murakawa, K., Ishida, S., Ishidashi, T., Takahashi-Fujii, A.,

Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.

Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.

Diversification of Transcriptional Modulation: Large-scale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu,
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Takao Isogai
FLJ Project (HRI Team)
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16344560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identification and Characterization of Putative Alternative Promoters of Human Genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: flj-cdna@nifty.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 81-438-52-3986
                             TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                                                                                                                                                   ACGCCTATAATCCCAGCACTTTGGGAGGCTGAGGCCGGTGGATCACCTGAGGTCAGGAGT 327
                                                                                                                                                                                                                                                                                                                                                                                 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                    CAAGATCGCACAACTGCACTCCAGCCTGGGTGACAGAGCCAAGACTCCGTCTCCCAAAAAA 147
                                                                                                                             TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                                                                                                                                                               TCAAGACCAGCCTGGCCAACACAGTGAAACCCCCATCTCTACTAAAAATACAAAAATTAGC 267
                                                                                                                                                                                                                                                                                        TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC 200
                                                                                                                                                                           TGGGCATGATGGTGCATGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGTTGCAGTGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TKIDN2012877"
/tissue_type="kidney, tumor_t
/clone_lib="TKIDN2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pME18SFL3"
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71.9%;
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Pred. No. 2.7e-18;
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DA808834/c
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AUTHORS
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Best Local Similarity
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1 (bases 1 to 581)

1 (bases 1 to 581)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,

Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,

Ishii, S., Sudyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,

Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,

Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,

Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.

Diversification of Transcriptional Modulation: Large-scale

Identification and Characterization of Putative Alternative

Promoters of Human Genes

Genome Res. 16 (1), 55-65 (2006)
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NEDO human cDNA project (New Energy and Industrial Technology

Developmental Organization, Japan); cDNA library construction:

Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,

Research Association for Biotechnology (RAB) and Biotechnology

Center, National Institute of Technology and Evaluation; 3'-end one

pass sequencing: RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                              CAAGATCGCACAACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCGTCTCCCAAAAAA 340
                                                                                                                                                                                                                                                                                                                      TCGAGACCATCCTGGCCAACATGGTGAAAACCCCGTCTTTACTAAAAATACAAAAAATAGC 200
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                                           САЛАЛАСАЛСАЛСАЛАЛАЛАСЛАЛАЛАЛ 347
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TAAATAAATAAATAAATAAAAATACA 313
                                                                                                                                            TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="brain"
/dev_stage="fetal"
/clone_lib="OCBBF3"
/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="OCBBF3024884"
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Pred. No. 2.7e-18;
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BM542252/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 418.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Eukaryota; Metazoa;
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1 (bases 1 to 1085)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                              CAAAAACAACAACAAAAAACAAAAAA 347
                                                                          CAAGATCGCACAACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCGTCTCCCAAAAAA 90
                                                                                                                                                                                                                                                                                                                  ACGCCTATAATCCCAGCACTTTGGGAGGCTGAGGCCGGTGGATCACCTGAGGTCAGGAGT
TAAATAAATAAATAAATAAAAATACA
                                                                                                               TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                                                        TGGGCATGATGGTGCATGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGTTGCAGTGAGC 150
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                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MCC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo of Average insert size 2 kb. Library constructed by Liff Technologies."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 2.4e-18;
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RESULT 24 AQ381551/c LOCUS

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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu/ordering) or from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Other GSSs: RPCIII-165E2.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence.
AQ381551
AQ381551.1 GI:4352574
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Venter,J.C.
Use of BAC End Sequences from Library RPCI.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                    CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG 143
                                                                                                                                                                                                                                                                           GCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGA
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                                                                                                                                                                                                                                                                                                                  AGACCAGCCTGGCCAACATGGTGAAACCCCCATTTCTACTAAAAATACAAAAATTAGCTGG
                                                                                 AAAAAAAAGAAAAGAAAAGAAAGAAAACATACACTGAAATTTTTAGGGGT 160
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/mol_type="genomic DNA"
/db_xref="GDB:7563073"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="RPCI-11-165E2"
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71.7%;
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e_lib="RPCI-11"
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Pred. No. 2.9e-18;
Nismatches 73;
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                        AAAAATAATAATAATAGAAAA
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                                                                                                                                                                                                                                                             TCAAGACTAGCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAATGAGT 526
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LOCUS
DEFINITION
                                                             Query Match
Best Local Similarity
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AGENCOURT 7860001 NIH_MGC_55 H
5', mRNA sequence.
EQ432755
EQ432755.1 GI:21171831
EST.
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Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2353 row: i column: 04
High quality sequence stop: 555.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
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1 (bases 1 to 775)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                          Conservative
                                                                                                                                                                                                                                                                    3' adaptor sequence:
5'-ANTOTAGAGGCCGAGGGGGGGGAGATG-dT(30)BN-3' (where B = A, C, G, or T). Average insert size C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Pal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
                                                           36.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type="mRNA"
                                                                                                                                              CA) . "
                                          0,
                                        Score 146.8; DB 3;
Pred. No. 2.7e-18;
0; Mismatches 72;
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AI753536/c
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Best Local S
Matches 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jia, L., Young, M.F., Powell, J., Yang, L., Ho, N.C., Hotchkiss, Robey, P.G. and Francomano, C.A.

Gene expression profile of human bone marrow stromal cells: high-throughput expressed sequence tag sequencing analysis Genomics 79 (1), 7-17 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing and analyses by National Institutes of Health Intramural Sequencing Center (NISC). Plate: 11 row: h column: 09
Seq primer: -21M13 forward primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Human Genome Research Institute 10/10C101, 9000 Rockville Pike, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Libin Jia
Medical Genetics Branch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: libin@helix.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 301-496-7157
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ATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAAA
                                                                                                                                                                                                                                  TGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAATAGCTGGGCATGGTGG
                                                                                                                                                                                                                                                                                 CCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACCGGAGGTCAGGAGTTCGAGACCAGCC
                                                                              CAGGCACCTGTAATCCCAGCTACTAGGGAGGCTTTTGAACCCAGGAGGCAGAGGTTGCAG
                                                                                                                             CACACACCTGTAGTCCCAGCTACTCAGGAG-----CCGGAGATTGCAGTGAGCTGAG
                                                                                                                                                                              TTGCCAACATAGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCCGGGCATGGTGG
                                                                                                                                                                                                                                                                                                                             CCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="HBMSC cr11h09"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="Human bone marrow stromal cells"
/note="Vector: pBluescript; Site 1: EcoRI, Site 2: XhoI;
/note="Vector: pBluescript; Site 1: EcoRI, Site 2: XhoI;
/note="Vector: pBluescript; Site 1: EcoRI, Site 2: XhoI;
/note="Vector: pBluescript; Site 2: XhoI;
/note="Vector: pBluescri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="bone marrow stroma"
/dev_stage="mixed"
/lab_host="XL1-Blue MRF'/SOLR"
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Pred. No. 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1365 Std Error: 0.00
Seq primer: -40UP from Gibco
Seq primer: -40UP from Gibco
High quality sequence stop: 297.
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National Cancer Institute, Cancer Genome Anatomy
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Mammalia; Eutheria;
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                                         CCGGAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAG
                                                                                                                                       AAAAATACAAAAATAGCTGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAG
                                                                                                                                                                                                                                                                                AGGCCAGGCACGTGGCTCATCCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGGGCGGA
                                                                                          AAAATACAAAATTAGCTGGGTGTGGTAGCACATGCCTGTAATCCCAGCTACTCGGGAG
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                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NCI_CGAP_Lym12"
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
SalI; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:2132539"
/tissue_type="lymphoma,
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Pred. No. 3.3e-18;
0; Mismatches 59;
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RESULT 29
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Best Local Sim
Matches 176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 667)
Pujjyama, A., Hattori, M., Toyoda, A., Taylor, T.D.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
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Pan troglodytes DNA, clone: RP43-020P17.T7,
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AG156377.1 GI:16686055
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                                                                                                                                     TGGGCATGGTGGCAGGCGCCTGTAGTCCCCAGCTACTCAGGAGGCTGAGGCAGGAGAGTTG
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R.Site 2
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/clone="RP43-020P17.T7"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Pan troglodytes"
/mol_type="genomic DNA"
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
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Matches 162; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l (bases 1 to 406)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Dias Neto, E., Garcia Correa, R., Zago, M.A., Bordin, S., Costa, F.F.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bata, G.S., Simpson, D.H.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Harc, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW902341 406 bp mRNA linear QV3-NN1023-130500-179-b08 NN1023 Homo sapiens cDNA, AW902341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                            TGAGATCG 268
                                                                                 TGGGCGTGGTGGGCACCTGTAGTCCCAGCTACTCAGGAGGCAGAGGTTGCGGTAAGC
                                                                                                                      TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                     TCGAGACCAGCCTGGCCAATATGGTGAAACCCCGTCTCTACTAAAAATTACAAAATTAGC
                                                                                                                                                                                                                                                        ACGCCTGTGATCCCAGCACTTTCAGAGGCCGAGGCAGGCGGATCACCTGAGGTCAGGAGT
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CGAGATAG 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
mol type="mRNA"
/db_xref="taxon:9606"
/dev stage="Adult"
/clone_lib="NN1023"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: nervous normal; Vector: pucl8; Site 1: SmaI; Site 2: SmaI; A mini-Tibrary was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Pred. No. 3.7e-18;
0; Mismatches 26
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Matches 209
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                                                                                                                                                                                       201 TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                                                390
                                                                                                                                                                                                                                                                  141 TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAAATACAAAAAAATAGC
                                         305
                                                                                 270
                                                                                                                                                                                                                                                                                                                             450
                                                                                                                                                                                                                                                                                                                                                                                                            209;
                                                                                                                                                                                                                                                                                                                                                  81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 461.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MdHHHALLE, HOMO.
HOMAINIALE, HOMO.
1 (bases 1 to 524)
1 (bases 1 to 524)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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AI302156.1 GI:3961502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI302156 524 bp mRNA linear EST 03-DEC-1998 qn58a05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1902416 3' similar to contains Alu repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAG------CA
                                                                                                                                                                                                                                                                                                                         CTTGAGCCTGGGAGGTGGAGGTTGCAGTGAGCCGAGACCGTGCCTCCAGCCTGGGTGACA
                                                                                                                                                            TGGGCATGGTGCTACACCTGTAGTCCCAGCTACTTGGGAGGCTGAGGTAGGAGAGTGG
                                                                                                                                                                                                                                            TCGAGACCAGCCTGGCCAACATGGTGAAACCCCCGTCTCTACTAAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NCI_CGAP_Kid5"
/clone_lib="NCI_CGAP_Kid5"
/note="Organ: kIdney; Vector: pT7T3D-PacI; Site_1: Not /note="Corn: 1st strand cDNA was primed with a Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xrefe"taxon:9606"
/clone="IMAGE:1902416"
/tissue_type="2_pooled_tumors_(clear_cell
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                           36.6%;
                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 146.4; DB 1
Pred. No. 3.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                        62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 524;
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CR860050
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TITLE
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1050
                                                                                             990
                                                                                                                                                                                   186;
                                                                                                                                       46 TAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCTGTAATCCCAGCACTTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuherberg, GERMANY

(Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Agowa (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZp470B1412) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp470B1412
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1459 bp mRNA linear HTC 12-NOV-200 Pongo pygmaeus mRNA; cDNA DKFZp470B1412 (from clone DKFZp470B1412) CR860050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The German cDNA Consortium Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae; Pongo.

1 (bases 1 to 1459)

Wambutt,R., Heubner,D., Mewes,H.W.,
Fobo,G., Han,M. and Wiemann,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pongo pygmaeus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CR860050.1
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AGGCCAAGGTGGGCGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGACCAACATGGA 1109
                                         AGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCATCCTGGCCAACATGGT 165
                                                                                          TAAGAAGCTGGATCTCCTGCCAGGCGCGCGTGGCTCATGCCTGTAATCCCACCACTTTGGG
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                    /translation="MKPILLQGHERSITQIKYNREGDLLFTVAKDPIVNVWYSVNGER
IGTYMGHTGAVWCUDADWDTKHVLTGSADNSCRLWDGETGKQLLLKYNSAVRFVGGFD
FGGSIIMFSTUDKQMGYQCFVSFFDLDFSQIDNDEPYMLFCNDSKITSAVWGPLGEO
IIAGHESGELNDKQMGYQCFVSFFDLWVKDHSRQINDIQLSRDMTWFVTASKDNTAKLFDST
TLEHQKTFRTERFVNSAALSENYDHVVLGGGGEMDVTTTSTXIGKFBARFFHLAFEE
EFGRVKGHFGLINSVAFHPDGKSYSSGGEDGYVRIHYFDPQYFEFEFEA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="DKFZD470B1412"
/clone=Tib="470 (synonym: pliv1). Vector pSport1_Sfi; host
/clone_Tib="470 (synonym: pliv1). Vector pSport1_Sfi; host
DH10B; sites SfilA + SfilB"
/dev_stage="adult"
/note="TGF-beta receptor interacting protein 1 (Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein"
/protein_id="CAH92198.1"
/db_xref="GI:55730962"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="DKFZp470B1412"
15. .992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="DKFZp470B1412"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1459
                                                                                                                                                                                                           36.6%;
                                                                                                                                                                                Score 146.4; DB 6
Pred. No. 2.9e-18;
D; Mismatches 66
                                                                                                                                                                                                                               DB 6;
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                                                                                                                                                                                     66;
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                                                                                                                                                                                                                                    1459;
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                                                                                                                                                                                   Gaps
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166 GAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCATGGTGGTGGCACACCACCTGTAG 225

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REFERENCE
AUTHORS
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ORGANISM
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Best Local Similarity
Matches 175; Conser
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  119
                                        261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brandenberger, R., Wei, H., Zhang, S., Li, Y., Xu, C., Fang, R., Guegler, K., Lebkowski, J and Stanton, L.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 650 473 8658 Fax: 650 473 7760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CN268905 302 bp mRNA linear EST 16-MAY 17000597786250 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 Constitution Drive, Menlo Park, CA 94025, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Geron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Brandenberger
Regenerative Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAGATCACAGA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATC 285
                                                                                                        TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                       TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTGAGCTGAGA 1241
CGTGAACCCGGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCGC
                                        TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGC
                                                                                   CGGGCGTGGTGGCGGGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGG
                                                                                                                                                                  TCAAGACCAGCCTGGCCAACATGGTGAAACCCCCGTCCTTACTACAAATACAAAAATTAGC
                                                                                                                                                                                                                                                   ACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTAGGCGGATCACCTGAGGTCAGGAGT
                                                                                                                                                                                                                                                                           ATGCCTGTAATCCCCAGCACTTCCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
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                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="GRN_PREHEP"
/note="oligo dT_primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type="embryonic stem cells, DMSO-treated
                                                                                                                                                                                                                                                                                                                                               36.6%;
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                                                                                                                                                                                                                                                                                                                                                 Score 146.2;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                   4.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rao, M.S., Murage, J., Fi
                                                                                                                                                                                                                                                                                                                                                                  DB 8;
                                                                                                                                                                                                                                                                                                                                48;
                                                                                                                                                                                                                                                                                                                                                                    Length 302;
                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                              Gaps
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141 TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC

ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140 ACGCCTGTAATCCTAGCACTTTGGGAGGCCGAGGCAGGTGGATCACCTGAGGTCAGGAGT

Matches Query Match Best Local

195;

Conservative

Similarity

36.6%;

Score 146.2; DB Pred. No. 4e-18; L; Mismatches

DB 3; 59;

Indels Length

4.

Gaps

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PUBMED COMMENT
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AUTHORS
TITLE
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SOURCE
ORGANISM
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BM712012/c
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
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University of Iowa
Joseph Grand
Joseph
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Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 419)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approximations are subtraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM712012
419 bp mRNA linear EST 28
UI-E-DW1-ahc-a-08-0-UI.r1 UI-E-DW1 Homo sapiens cDNA clone
UI-E-DW1-ahc-a-08-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM712012.1 GI:19025270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence: 1-181,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          discovery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.
                         /dev stage="adult"
//dev stage="adult"
//lab_host="DH10B (Life Technologies) (TI phage resistant)"
//clone_lib="UI-E-DM1"
//clone_lib="UI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-DW1-ahc-a-08-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .419
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RESULT 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEYWORDS
                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BRSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
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                                201
                                                                  377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Geron Corporation
230 Constitution Drive, Menlo Park,
Tel: 650 473 8658
Fax: 650 473 7760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.

Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CN351916 68
17000532267149 GRN_EB Homo
CN351916
CN351916.1 GI:47351850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: rbrandenberger@geron.com
Insert Length: 680 Std Error: 0.00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Regenerative Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae; Homo.
1 (bases 1 to 680)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Brandenberger R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15146197
                  TGGGCATGGTGGCACACACCTGTAGTCCCCAGCTACTCAGGAGCCGGAGATTGCAG 255
                                                                                    TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                ATGCCTGTAATCCCAGCACTTTGGGAGGCCAAAGTGGGCAGATCACCTGAGGTCAGGAGT
                                                                                                                                                     ATGCCTGTAATCCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
                                                                 TCGAGACCAGCCTGGCCAACATGGTGAAAACCCCGTCTACTAAAAAATACAAAAATTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    СААЛААСААСААСААЛАЛА 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGAGACCAGCCTGGCCAACATGGTGAAACTCCATCTCTACTAAAAATACAGAAATTAGC
 TGGGCATGGTGGCGCACACCTGTAATCCCCAGCTACTCCGAAGGCTGAGGCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGTATGGTGGTGCATGCCTGTAATCCCAGCTACTAGGGAGGCTGAGGCAGGAGAATCA
                                                                                                                                                                                                Conservative,
                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"

/mol type="mRNA"

/mol type="mRNA"

/mol type="mRNA"

/db_xref="taxon:9606"

/tissue_type="embryonic stem cells, embryoid bodies

derived_from H1, H7 and H9 cells"

/clone_lib="GRN_EB"

/note="filipg dT primed, full-length enriched cDNA library

from embryoid body outgrowths derived from hES cell lines

H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                               36.6%;
                                                                                                                                                                                                <u>,</u>
                                                                                                                                                                                                            Score 146.2; DB 8
Pred. No. 3.7e-18;
                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  680
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                                                                                                                                                                                                Indels
                                                                                                                                                                                                                               Length
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SOURCE
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BE379282/c
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                       81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGGGGGATCACCTGAGGTCAAGAGA 140
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM265 row: i column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 685)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence start: 4 High quality sequence stop: 634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
BE379282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE379282 685 bp mRNA linear EST 21-JUL-2000 601237929F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3610063 5';
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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CAAAAAGAAAAGAAAAA
                                                                                                                                                                                                                    TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                        CAAAAACAACAACAAAAA 339
                                                                                    CTTGAACCCAGAAGGTGAAGGGCACAGTGACC--
                                                                                                                               TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                                                                                                                                                                                                             TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                                   TCGAGACCAGCCTGGCCAACATGGTGAAACTCCATCTCTACTAAAAAATACAGAAATTAGC
                                                                                                                                                                                                                                                                                                                                                             ACGCCTGTAATCCTAGCACTTTGGGAGGCCGAGGCAGGTGGATCACCTGAGGTCAGGAGT 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B (phage-resistant)"
/clone lib="NJH MGC 44"
/clone lib="NJH MGC 44"
/clone lib="NJH MGC 44"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Si
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .685
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mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.6%;
93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 146.2; DB 7
Pred. No. 3.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                       AGGCGCCAGAGTGAGACTCTGTCT
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CN411940/c
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Best Local Similarity
Matches 195; Conserv
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323 bp mRNA linear EST 24-FEB-1998 od36h04.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1370071 similar to contains Alu repetitive element;contains element PTR5 repetitive element;, mRNA sequence.

AA836548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17000532275949 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
CN411940
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Tel: 650 473 8658
Fax: 650 473 7760
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rbrandenberger@geron.com
Insert Length: 805 Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Geron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Regenerative Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Brandenberger R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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                                                                                                                                                         CAAAAACAACAACAAAAA 339
                                                                                                                                                                                             CTTGAACCCAGAAGGTGAAGGCACAGTGACC----AGGCGCCAGAGTGAGACTCTGTCT
                                                                                                                                                                                                                   TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGAGTGAGACKCCGTCT
                                                                                                                                                                                                                                                                                        TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
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                                                                                                                                       CAAAAGAAAAAGAAAAA
                                                                                                                                                                                                                                                              TGGGTATGGTGCATGCCTGTAATCCCAGCTACTAGGGAGGCTGAGGCAGGAGAATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="GRN_ES"
/note="oligo dT primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="embryonic stem cells, cell lines H1, H7, and H9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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75.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 146.2; DB 8; Pred. No. 3.6e-18;
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Best Local Similarity
Matches 206; Conserv
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                                                                                                                                                                                                                                                                                                              81
44
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CSAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cqapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., I
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae; Homo.
1 (bases 1 to 323)
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                                                                                                                                                                                                                             TCGAGACCATCCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
                       CKCCGTCTCAAAAACAACAACAACAAAAAAAAA 343
                                                                                                                                                                                                                                                                            ATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGNCAGGTCGCCTGAGGTCAGGAGT
                                                                                                                                                                                                                                                                                                ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                  CTTGAACCCAGAAGGCGGAGGTTGCAGTGAGCCGAGATCAACCTGGGAGACAGAATGAGA
                                                                                                    --TGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAG-CAGAGTGAGA
                                                                                                                                                                       TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAG----
                                                                                                                                                                                                           TGGAGACCAGCCTGGCCAACATGGCAAAAACCTGTCTCTACTAAAAAATACAAAAATTAGC
                                                                                                                                       TGGGTGTGGTGGTGCATGCCTGTAATCCCAGCTTCTCGGGAGGCTGAGGTAGGAGAATCA 105
                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:1370071"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:2910867
                                                                                                                                                                                                                                                                                                                                                               36.4%;
                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                Score 145.6; DB 1
Pred. No. 5.5e-18;
L; Mismatches 56
   14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endocrine Pancreas Consortium 
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 617-495-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3', mRNA sequence.
BQ267427
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1 (bases 1 to 416)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                            ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                         TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                   TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                   ACGCCTGTAATCCTAGCACTTTGGGAGGCCAAGGTGGGCAGATCACCTGAGGTCAGGAGT
                                                                                       TCGAGACCAGCCTGACCAATATGATGAAACCCCCGTCTCTA-AAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  617-495-8557
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                        (http://genome.wustl.edu/est/lambda protocol.shtml). Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Pern Laboratory, Washington University School of Medicine, 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this a Washington University Pancreas EST project library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: pancreas; Vector: pBluescript SK-; Site_1: XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to pBluescript SK- by Dr. H. Inoue following the Washington University protocol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="taxon:9606"
/clone="IMAGE:5780494"
/tissue_type="insulinoma"
/lab host="PH10B (phage-resistant)"
/clone_lib="Human insulinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
|mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                 36.4%;
78.0%;
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Pred. No. 5.7e-18;
1; Mismatches 47;
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97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seatt
Tel: (206) 616-3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ598684 464 bp DNA linear GSS 08-JUN HS_5336_B2_E09_SP6E RPCI-11 Human Male BAC Library Homo sapien genomic clone Plate=912 Col=18 Row=J, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence-tagged connectors: A sequence approach to mapping scanning the human genome
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1 (bases 1 to 464)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 464.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.htsc.washington.edu
Plate: 912 row: J column: 18
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Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: BAC ends
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ATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACCTGAGGTCAGAAGC 156
                                          ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
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                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          jwallace@u.washington.edu
                                                                                                                                                                                                               /clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen do
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
                                                                                                                                                                                                 pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                    sex="male"
                                                                                                                                                                                                                                                                                                                                                         clone="Plate=912 Col=18 Row=J"
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                                                                                                      36.4%;
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                                                                               Score 145.4; DB 11,
Pred. No. 5.6e-18;
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Human Male BAC Library Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing
Washington University Genome Sequencing Center For informati
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestealli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Walliams,T., Jackson,Y. and Bowers,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ269776 518 bp mRNA linear EST 15-JUL-2003 ik30a05.x1 HR85 islet Homo sapiens cDNA clone IMAGE:5782185 3' similar to SW:ALU7 HUMAN P39194 ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY. [1]; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Possible reversed clone: similarity Seq primer: -40UP from Gibco
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Endocrine Pancreas Consortium
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     /lab nost="univ"
/clone lib="HR85 islet"
/clone lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~lkb. 5;
XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Buclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                        tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
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DA175472
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1 (bases 1 to 551)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Kimura, K., Wakamatsu, A., Sekine, M., Tsuritani, K., Wakaguri, H., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yokoi, T., Kondo, H., Wagatsuma, M. Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M. Murakawa, K., Ishida, K., Kandahi, T., Takahashi, Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification and Characterization of Putative Alternative Processing Constitutions and Characterization of Putative Alternative
                                                                                                                                                                                                                                                               Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction:

Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology
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                                                                                                                                                                                                                     Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                          Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Takao Isogai
FLJ Project (HRI Team)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 81-438-52-3975
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                  /tissue_type="amygdala"
/clone_lib="BRAMY2"
/note="Vector: pME18SFL
                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                      organism="Homo sapiens
                                                                                      clone="BRAMY2038827"
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Pred. No. 5.5e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201
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                                                                                         24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81
                                                                                                                                                                                                                                                                                                                                                                                                          Henan Bioengineering Key Lab
Henan Normal University
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liver regeneration after Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                Email: xucs@x263.net.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Cun-Shuan Xu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xu, C.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DW412368.1 GI:84913924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens cDNA, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HHAGE013098 Human liver regeneration
                                           TGGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAAATAGC
                                                                                                        ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGA------GCCGGAGATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGGCATGATGGTGCATGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGTTGCAGTGAGC
                            TCGAGACCAGCCTGGTCAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAACTAGC
                                                                                       TAAATAAATAAATAAAATAAAATACA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAGATCGCACAACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCGTCTCCCAAAAAA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAAGACCAGCCTGGCCAACACAGTGAACCCCCATCTCTACTAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
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                                                                                                                                                                                                                                                                                                                                                                              148 Jianshe Road, Xinxiang City, P.R.China : 00863733328084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 324)
                                                                                                                                                                                                                                                                                                                                                                00863733326524
                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol type="mRNA"
/db xref="reaxon:9606"
/tissue_type="liver"
/clone_lib="Human liver regeneration after partial
                                                                                                                                                                                                                         nepatectomy"
                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                              36.3%;
71.1%;
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71.5%;
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                                                                                                                                                Score 145.2; DB 10,
Pred. No. 6.6e-18;
D; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 145.4; DB 9
Pred. No. 5.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PH
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                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA linear
after partial
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                                                                                                                                                 Indels
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                          143
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REFERENCE
AUTHORS
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KEYWORDS
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DB330188/c
                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
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                                                                                                                                                                             Matches
                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
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                                                                                      341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254
                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae; Homo.

1 (bases 1 to 498)

1 (bases 1 to 498)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,

Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,

Tahii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,

Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,

Yoneyama, T., Otsuka, R., Kanda, K., Tsoo, Y., Irie, R., Wagatsuma, N.,

Yoneyama, T., Otsuka, R., Kanda, K., Tsoo, Y., Irie, R., Wagatsuma, N.,

Yoneyama, T., Wagatsuma, N., Yakahashi-Fujii, A.,

Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,

Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S

Diversification of Transcriptional Modulation: Large-scale

Identification and Characterization of Putative Alternative

Promoters of Human Genes

Genome Res. 16 (1), 55-65 (2006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
DB330188
DB330188.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japani; cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16344560
Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB330188
DB330188 PROST2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2-6-7 Kazusa-Kamatari, Kisarazu, Chiba,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                      CAGGCATGACACTGGCTGAATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGG 121
CAGGTACTCAGCCATGTGCTGGGCCATGGGAACCCCAAATATTAATAAGACATTGTCAGGC
                                                                                      CATTTTCTCATGCATCTATTGGTCATTTGTACATCTCTTGAGAAAATGTCTTAAAAAA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTGAACCTGGGAGGCAGAGGTTGCAACCATTGCACTCCAGCCTGGGCGACAAGAGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGAGCGTGGTGCACGCTTGTAATCCCCAGCTACTCGGGAGGCTGAGGCAGGAGAAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KCCGTCTCAAAAACAACAACAAAAAAACAAAAAAACCATAAGACATTGTCCATCT 367
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="pROST2015815"
/tissue type="prostate"
/clone_Tib="pROST2"
                                                                                                                                                                                                                                                                               note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          . .498
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                                                                                                                                                                                             36.3%;
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                                                                                                                                                                        0,
                                                                                                                                                                      Score 145.2; DB 9;
Pred. No. 6.1e-18;
0; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA
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                                                                                                                                                                                                               Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 10-DEC-2005
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                                                                                                                                                                        Gaps
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222
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FUBMED COMMENT
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AUTHORS
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 44
DA714821/c
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                                                                             Matches
                                                                                                                  Query Match
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                                                                                                   Local
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                                    81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 515)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,

Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,

Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,

Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,

Murakawa, K., Ishidashi, T., Takahashi-Fujii, A.,

Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.

Diversification of Transcriptional Modulation: Large-scale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); CDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DA714821 DA714821 NT2RI2 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: flj-cdna@nifty.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 16 (1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Promoters of Human Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identification and Characterization of Putative Alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAAAATTACAAAATTAGCTGGGCGTGGTGGCGAGTGCCTGTAATCCCAGCTACTCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAAAAATACAAAAAAATAGCTGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCACCTGAGGTCAGGAGTTTGAGACCAGTCTGGCCAACATGGTGAAACCCCGGTCTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCACCTGAGGTCAAGAGATCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTAC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCTGAGACTGGGTTCATTTGA
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                                  ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81-438-52-3975
                                                                             Conservative
                                                                                                                                                                                 /note="Vector: pME18SFL3; majorly NT2 neuron; mRNA from
NT2 neuronal precursor cells treated 2-weeks mitotic
inhibitor after 5-weeks retinoic acid (RA) induction."
                                                                                                                                                                                                                                                                   /cell_type="teratocarcinoma"
/cell_line="NT2"
                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                               clone
                                                                                                                                                                                                                                                                                                            clone="NT2RI2021923"
                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:82370722
                                                                                               36.3%;
                                                                                                                                                                                                                                             _lib="NT2RI2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55-65
                                                                           0;
                                                                           Pred. No. 6e-
); Mismatches
                                                                                                 Score 145.2;
Pred. No. 6e
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cDNA clone
                                                                           48;
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NT2RI2021923
                                                                                                                  Length
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5', mRNA
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                                                                             Gaps
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ACCESSION
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AQ314853/c
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ORGANISM
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                                                                                                                                                                                              Query Match
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                                                                                                                                                                               Best Local Similarity
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                                       144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other GSSs: RPCI11-96D8.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0206
Clones are derived from the human BAC library RPCI-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ314853.1 GI:4046316
GSS.
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RPCI11-96D8.TV RPCI-11 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAGATCGCACAACTGCACTCCAGCCTGGGTGACAGAGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAAATACAAAAAAATAGC
                           AGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAAATAGCTGG
                                                                             CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG 143
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  AGACCAGCCTGGCCAACATGGTGAAACACCATCTCTACTAAAAATACAAAAATTAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 555)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens (human)
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                              /note="Vector: pBACe3.6; Site_1:
RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                 /cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6;
                                                                                                                                                                                                                                                                                                                                                            /db_xref="GDB:7536559"
/db_xref="taxon:9606"
/clone="RPCI-11-96D8"
                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              .555
                                                                                                                                                                               36.3%;
                                                                                                                                                          Score 145.2; DB 11; Pred. No. 5.9e-18; 1; Mismatches 59;
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genomic clone RPCI-11-96D8,
                                                                                                                                                                                                  DB 11;
                                                                                                                                                                                                                                                                                     EcoRI; Site
                                                                                                                                                              Indels
                                                                                                                                                                                                Length
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TITLE
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                                                                                                                                                                                  Query Match
Best Local S
Matches 162
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                        162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       591 bp
AGENCOURT 11828537 NICHD Rh_Ov1
IWAGE:6913528 5', mRNA sequence.
CB309712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLM3154 row: m column: 15
High quality sequence stop: 454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Eliot Spindel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macaca mulatta
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                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: CLONTECH
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI_CGAP clone distribution information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATCGCAG------AGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTG
                                                                                                                 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                       ATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGGGCAGATCACTTGAGGACAGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGACKCCGTCTCAAAAACAACAACAAAAAAAACAAAAAAA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAACCCAGGAGGCGGAGGTTGCAGTGAGCCGAGATCACGCCACTGCATTCCAGTCCAGTG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGTGGTGACGCGCACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGACTCCGTCTCAAAAAAAAAAAAAGTAAGTTAATTAA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 591)
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                          /tissue_type="Ovary"
/lab host="PH10B (phage-resistant)"
/lab host="PH10B (phage-resistant)"
/clone_libe="NICHD Rh_Ov1"
/note="Torgan: ovary; Vector: pDNR-LIB; Site 1: Sfi I;
/note="Torgan: ovary; Vector: pDNR-LIB; Site 1: Oligo
Site 2: Sfi I; Cloned unidirectionally. Primer: Oligo
Average insert size 1.0-4.0 kb. Tissue pooled from
pre-pubertal, post pubertal sn menopausal monkeys.
Constructed by Clontech. Note: this is a NICHD Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="IMAGE: 6913528"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Macaca mulatta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                   36.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             xref="taxon:9544"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _type="mRNA"
                                                                                                                                                                                  0;
                                                                                                                                                                              Score 145.2; DB 4;
Pred. No. 5.9e-18;
0; Mismatches 29;
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clone
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ACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGC 205

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KEYWORDS
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DA408951
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Best Local Similarity
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                                                                                       273 CCTGGACAACTCCCTCTATAAGAAATAGAAAAATGAGGCCAGGCACATGGCTCATGTC
                                                                                                                                                                                195;
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                                                                                                                               26 CATGGGAACCCAAATATTAATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology

NEDO human cDNA project (New Energy and Industrial Technology

Developmental Organization, Japan); cDNA library construction:

Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,

Research Association for Biotechnology (RAB) and Biotechnology

Center, National Institute of Technology and Evaluation; 3'-end opass sequencing: RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I (bases 1 to 649)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,

Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,

Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,

Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,

Murakawa, K., Ishida, S., Ishibashi, T. Takahashi-Pujii, A.,

Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.

Diversification of Transcriptional Modulation: Large-scale

Identification and Characterization of Putative Alternative

promoters of Human Genes

Genome Res. 16 (1), 55-65 (2006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba,
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Takao Isogai
FLJ Project (HRI Team)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo
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                              TGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAG 145
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  TGTAATCTCAGCACTTCGGGAGGCTGAGGTGAGCAGATCACTTGAGGTCAGGAGTTCGAG
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                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="BRTHA3015134"
/tissue type="thalamus"
/clone_Tib="BRTHA3"
                                                                                                                                                                                                                                                                                           /clone_lib="BR'
/note="Vector:
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                                                                                                                                                                                                 Score 145.2; DB 9;
Pred. No. 5.8e-18;
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                                                                                                                                                                              Mismatches
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                                                                                                                                                                            Gaps
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392
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CZ459725
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Best Local
Matches 20
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                   204 GCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGA
                                                                                                                                                 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Decoding the genomic architecture and high throughput detection of fusion transcripts in breast cancer cell lines: implications for a tumor genome project Unpublished (2005)
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MCF748c16TF Human MCF7 breast ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.genomex.com
Class: BAC ends.
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Volik,S.V., Raphael,B.J., Huang,G.-Q., Murnane,J., Brebner,J.H.,
Bajsarowicz,K., Paris,P., Tao,Q., Kowbel,D., Lapuk,A.V., Kuo,W.-L.,
Shagin,D.A., Shagina,I.A., Magrane,G., Gray,J.W., Jan,F.-C., de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Volik SV
Colin Collins' lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jong, P., Pevzner, P. and Collins, C.
                                                                                                AGACCATCCTGGCCAACATGGTGAAAACCCCGTCTTTACTAAAAATACAAAAAAATAGCTGG
                                                                                                                                                                     CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG
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                                                                                                                                                 CCTGTAATCCCAGCACTTTGGGAGGCCGAGGCAGGCGGATCACCTGAGGTCAGGAGTTCG
GCGTGGTGACGCGCACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAAGAATCGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l: svolik@cc.ucsf.edu
clone is available from Amplicon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Comprehensive Cancer Center
Box 0808, San Francisco, CA
415 502 7066
415 502 5665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens (human)
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                              /note="Vector: pECBAC1; Site_1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 (clone lib="Human MCF7 breast cancer cell line library
(MCF7 ī)"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="MCF7_48c16"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DN/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
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Pred. No. 5.5e-18;
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DA112846
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VERSION
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DA112846
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1 (bases 1 to 550)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Kimura, K., Wakamatsu, A., Sekine, M., Tsuritani, K., Wakaguri, H., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Kushida, N., Ishila, S., Sugiyama, T., Saito, K., Isono, Y., Irle, R., Kushida, N., Yoneyama, T., Oteuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, Yoneyama, T., Oteuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helix Research Institute
2-6-7 Kazusa-Kamatari, Ki
Tel: 81-438-52-3975
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DA112846.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
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                               GCTGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGA 258
                                                                                           TTTGAGACCAGCCTGGCCAACATGGTGAAAACCCCATCTCTACTAAAAATCACAAAAATTA 369
                                                                                                                                    ATCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAAT-ACAAAAATA 198
                                                                                                                                                                                  ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCA-CCTGAGGTCAAGAG 139
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  GCCAGGCGTGGTGATGCACACCTGTAATCCCAGCTACTCGGGAGGTGGAGGTTGCAGTGA
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BRACE3 Homo sapiens
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ACCESSION VERSION KEYWORDS JOURNAL PUBMED COMMENT AUTHORS RESULT 50 DA198015/c 밁 9 문 ORIGIN FRATURES SOURCE DEFINITION Query Match
Best Local Similarity
Matches 157; Conserv TITLE ORGANISM source 487 201 427 141 482 319 430 259 18 I (bases 1 to 555)

Rimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Thujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006) DA198015 DA198015 Email: flj-cdna@nifty.com
MEDO human cDNA project (New Energy and Industrial Technology
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB Fax: 81-438-52-3986 Helix Research Institute 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan Contact: Takao Isogai FLJ Project (HRI Team) 16344560 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens DA198015.1 GI:78309617 Bequence. DA198015 Tel: 81-438-52-3975 Hominidae; Homo Homo sapiens (human) ATGCCTGTAATCCCAGCACTTTGGGAGGCCAAAGTGGGCAGATCACCTGAGGTCAGGAGT TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGACCGGAGATTGCAGTG 257 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140 GCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGACAGAGTGAGACKCCGT TCGAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTACTAAAAAATACAAAAATTAGC ТССВАСАССАТССТССССАЛСАТССТСВАЛАЛССССССТСТТТАСТАЛАЛАТАСЛАЛАЛАЛАГАСС 200 CTCAAAAAACAAAAAAAAAAAAAACAACGAGCAAACCATGGTCC 526 СТСАРАРАССАР САРАВАРАРАРАРАРА В СЕТТАР САСТТСТСС 363 ĠĊĊĠĀĠĀŤĊĠĊĀ-----Conservative /organism="Homo sapiens"
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/db xref="taxon:9606"
/clone="BRAWH2000862"
/tissue type="brain"
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Db 367 CGGGCATGGTGGCGCACACCTGTAATCCCAGCTACTCCGAAGGCTGAGGCAGGAGAG 311

Search completed: July 17, 2006, 22:20:11 Job time: 4693 secs

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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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PAPELICANT VENTER, J. Craig et al.
APPLICANT VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 00/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-10-03
PRIOR FIL
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; ORGANISM: Human
US-09-949-016-192208
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 192208
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: VENTER, J.
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Patent No. 681233
                                                                                                                                                                                                                                                   Query Match 39.6%;
Best Local Similarity 73.9%;
Matches 201; Conservative
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Best Local Similarity
                                     136 AGAGATCGAGACCATCCTGGCCAACATGGTGAAACCCCGGTCTTTACTAAAAAATACAAAAA
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                                                                                                                                                                                                                                                          Score 158.4; DB Pred. No. 9e-37; 0; Mismatches
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RESULT 4
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US-09-949-016-12783/c
PACENT NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
                                                                                                                                                         Sequence 17230, A Patent No. 681233
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SEQ ID NO 12783
LENGTH: 15564
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Matches 201; Conservative
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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CURRENT FILING DATE: 2000-04-14
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NUMBER OF SEQ ID NOS: 207012
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                            CGTCTCAAAAACAACAACAAAAAACAAAAAAA 347
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Pred. No. 1e-
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1e-36;
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Sequence 13909,

Application US/09949016

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RESULT 5
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; ORGANISM: Human
US-09-949-016-17230
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Best Local Similarity
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                                                          10337
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                                                                                                                                                             TGAGATCGCAG-----AGTGAGCCGAAATCACAGATCACAGAGTGAGCAGA 306
                                                                                                                                                                                                              TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
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                                                                                                                            CTTGAACCCAGGCGGCGGAGGTTGCAGTGAGCCGAGATCGCACCAGCTTGGGTGACAAGC 10456
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Pred. No. 2.1e-36;
1; Mismatches 57
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밁 Ś ; ORGANISM: Human US-09-949-016-13909 PATENT NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14 SOFTWARE: FastSEQ SEQ ID NO 13909 Query Match Best Local Similarity PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012 ENGTH: 14253 DNA 200; 81 44789 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGATCACCTGAGGTCAAGAGA 140 ATGCCTGTAATCCTGGCACTTTGGGAGGCCAAGGCGTGTGGATCATTTGCGGTCAGGAGT 14312 Conservative 38.6%; 0, Version Score 154.4; DB 3; Pred. No. 2.4e-35; D; Mismatches 76; Length Indels 44789; 0. Gaps

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US 09-949-016-17302/c; Sequence 17302, Appl: ; Patent No. 6812339; GENERAL INFORMATION:
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US-09-949-016-12542/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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ORGANISM: Human
-09-949-016-12542
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6812339
APPLICANT: VENTER, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
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les 203; Conserv
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                                                                                                                                                                                                                                   САЛАЛАСАЛСАЛСАЛАЛАЛАСАЛАЛ 344
                                                                                                                                                                                                                                                                                                                               TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
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                                                                 Application US/09949016
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Craig et al
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Pred. No. 4.2e-35;
1; Mismatches 52;
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OF DETECTION AND USES THEREOF
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FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASESEQ for Windows Version 4.0

SEQ ID NO 17302
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US-09-949-016-15580/c
; Sequence 15580, Application US/09949016
; Patent No. 6812339
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DN
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les 203; Conserv
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                                                                                                                                                                                                                        TGAGATC-----ATGCCACTGCACTCCAGCCTGGGCGACAAGAGCAAAACTCCATCT 18142
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Pred. No. 4.2e-35;
1; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 173791;
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; OTHER INFORMATION: n = A, T, C
US-09-949-016-15580 .
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version SEQ ID NO 15580
                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 207012
                                                  NAME/KEY: misc_feature LOCATION: (1)...(71574)
                                                                                                                           ORGANISM: Human
                                                                                                                                                        TYPE: DNA
                                                                                                     FEATURE:
                                                                                                                                                                                 ENGTH:
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OF DETECTION AND
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 38.4%;
Best Local Similarity 69.8%;
Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 12683
LENGTH: 152524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6812339
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Human
-09-949-016-12683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION FILE REFERENCE: CL001307
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23608 CGAAAGTTGCAGTGAGCCGAGGTCGTGCCACTGCGACAGAGCAGAGCTCTGTCTCAAAAA 23549
                                                                                                                                                                                                                                                                                                                         23848 CTAATTCCAAAATAAAATTCTTÄACTCCTGCÄGGGCAGTGGCTCÄCGCCTGTÄÄTCCCÄ
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                                                                                                                                                                                                                                                              GCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCATCCTGG
                                                                                                                                                                                                                                           GCACTTTGGGAGGCTGAGGTGGATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGG
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                                   AGCCGAAATCACAGATCACAGAGTGAG-----CAGAGTGAGACKCCGTCTCAAAAA 326
                                                                             ATGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGAAGAATGGCTTGAACCCGGGAGG
                                                                                                                    ACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAGATCGCAGAGTG
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72.8%;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 153.4; DB 3; Pred. No. 7.9e-35; 1; Mismatches 87;
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Pred. No. 5.1e-35;
0; Mismatches 74;
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RESULT 11
US-09-949-016-16011/c
; Sequence 16011, Application US/09949016
; Patent No. 6812339
; Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS (
FILE REFERENCE: CL001307
CURRENT FAPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20

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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001307
CURRENT PELLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version SEQ ID NO 13194
LENGTH: 152524
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PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
mes 224; Conserv
                                                                        23608
23548
                                                                                                                                                   23668
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                                                                                                                                                                                                                                                                                                    23788 GCACTTTGGGAGGCTGAGGTGGGTCACCTGAGGTCAGGAGTTCGAGACCAGCCTGG
                                                                                                                                                                                                                                                                                                                                                                               23848 CTAATTCCAAAATAAAATTCTTAACTCCTGCAGGGGCAGTGGCTCACGCCTGTAATCCCA
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                                                                                                                                                                                                                                                                                                                                          96 GCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCATCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                   36 CAPATATTAPATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCTGTAATCCCA 95
                                                                        CGAAAGTTGCAGTGAGCCGAGGTCGTGCCACTGCGACAGAGCAAGACTCTGTCTCAAAAA
CAACAACAACAACAACAA 23528
                                 CAACAACAAAAAACAAAAAA 347
                                                                                                                                                   ATGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGAAGAATGGCTTGAACCCGGGAGG
                                                                                                                                                                                                                                                         CCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCATGGTGGCAC
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                                                                                                              AGCCGAAATCACAGATCACAGAGTGAG-----
                                                                                                                                                                         ACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGCTGAGATCGCAGAGTG
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Pred. No. 7.9e-35;
1; Mismatches 87
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                                                                                                  -CAGAGTGAGACKCCGTCTCAAAAA 326
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US-09-949-016-69587/c
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PRIOR FILING DATE: 2000-10-20
| PRIOR APPLICATION UVMBER: 60/237,768
| PRIOR FILING DATE: 2000-10-03
| PRIOR APPLICATION UVMBER: 60/231,498
| PRIOR FILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                  Query Match
Best Local S
Matches 225
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CLOO1307

CURRENT APPLICATION UNDER: US/09/949,016

CURRENT FILLING DATE: 2000-04-14

CURRENT FILLING DATE: 2000-04-14
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Matches 219; Conserv
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LENGTH: 40091
                                                                                                                                                                                                                                                                                 SEQ ID NO 69587
LENGTH: 601
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Patent No. 6812339
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Human
-09-949-016-69587
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                                                                                                                                                                     Similarity
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                                                                                                                 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
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                                                                          ACGCCTGTAATCCCAGCACTTTGGGAGGCTAAGGTGGGCGGATCACCTGAGGTCAGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAACAACAACAAAAAAAAAAAACCATAAGACATTGTCCATCTGCGGTTCC
     TCGAGACCAGCCTGGCCAACATGGTGAAAACCCTGTCTACTAAAAATACAAAAATTAGC
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                                                                                                                                                Score 152; DB 3; L
Pred. No. 2.2e-35;
2; Mismatches 57;
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APPLICANT: VENITER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 12784
LENGTH: 17050
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Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          Matches 201;
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                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(17050)
OTHER INFORMATION: n = A,T,C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
11706
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                                                                                                                                            CGCACGTGGTGGCGCGCCTGTAATCCCAGCTACTCGGGAGGCGGAGGTTGCAGCGAGC
                                                                                                                                                                                                                                            TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAAATACAAAAAATAGC
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                                                                                                   TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                 CAAAAACAACAACAAAAAAAACAAA 343
                                                                     AGAGATCGTGCCATTGCACTCCAGTCTGGGCGA-----
                                                                                                                                                                 TGGGCATGGTGGCACACACCTGTAGTCCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
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pred. No. 1.3e-34;
1; Mismatches 52;
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OF DETECTION AND
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/241,755
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US-09-949-016-13784
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APPLICANT: VENTER, J.
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13784, Application US/09949016 Patent No. 6812339
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Best Local Similarity
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FEATURE:
PAME/KEY: misc_feature
LOCATION: (1) ... (17050)
OTHER INFORMATION: n = A,T,C or
-09-949-016-13680
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APPLICANT: VENTER, J.
                                                                                                                                                                                                                                    FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                             APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PELICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 
EQ ID NO 13680 
LENGTH: 17050
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nilarity 76.4%;
Conservative
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Pred. No. 1.3e-34;
1; Mismatches 52;
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; LENGTH: 19566
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12096
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                                                Query Match
Best Local Similarity. 72.1
                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12096, Ap
Patent No. 6812339
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Matches 225; Conserv
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                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012
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LOCATION: (1)...(20099)
OTHER INFORMATION: n = A,T,C
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TYPE: DNA
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                             ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
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                                                              Score 150.4; DB 3;
Pred. No. 2.7e-34;
0; Mismatches 76;
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l; Mismatches 58
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                                                                                             Length 19566;
                                                                 Indels
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Sequence 14157, Application U. Patent No. 6812339 ; GENERAL INFORMATION: APPLICANT: VENTER, J. Craig of TITLE OF INVENTION: WITH HUITTILE OF INVENTION: WITH HUITTILE OF INVENTION:
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US-09-949-016-14114/c
                                                                                                                                               US-09-949-016-14157
                                                                                                                                                                        RESULT 18
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Patent No. 6812339
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION.
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Human
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LENGTH: 19567
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J. Craig et al.
POLYMORPHISMS IN KNOWN GENES
WITH HUMAN DISEASE, METHODS
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       ASSOCIATED
OF DETECTION AND USES THEREOF
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                                                                                                                                       SOFTWARE: FASTSEQ
SEQ ID NO 11940
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11940,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
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LOCATION: (1)...(45572
OTHER INFORMATION: n =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
NAME/KEY: misc_feature
LOCATION: (1)...(481115)
OTHER INFORMATION: n = A,T,C
                                                           TYPE: DNA
ORGANISM: Human
FEATURE:
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1; Mismatches 6
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Query Match

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Best Local Similarity
Matches 205; Conserv
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LENGTH: 157822
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001107
FILE REFERENCE: CL001107
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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TYPE: DNA
ORGANISM: Human
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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                                             TGAGATTGCACCACTGCTCTTTAGCCTGGGTGA----
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73.5%;
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Pred. No. 1.2e-33;
1; Mismatches 62;
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Pred. No. 1.7e-33;
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                                             ----CAGAGCAAGACTCTGTCT
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498
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Matches 236; Conservat
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)...(228896)
OTHER INFORMATION: n = A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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KCCGTCTCAAAAACAACAACAAAAAACAAAAAACCATAAGACAT
                                                                    AGTGAGCTGAGATCACCACCTGCACTCCAGCCTGGAGGGGGGGTGGGGGCAGAGCAAGAC
                                                                                                                                                                                                                                               GAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCATGGTGGCACACACCTGTAG
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                                                                                                     AGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGAC
                                                                                                                                        TCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATTGCTTGAACTCAGGAGGCAGAGGTTGC
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Pred. No. 1.9e-33;
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RESULT 22
US-09-949-016-12517/c
US-09-949-016-12517, Application US/09949016
Sequence 12517, Application US/09949016
Patent NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES AS:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14

ASSOCIATED OF DETECTION AND

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US-09-949-016-16021/c
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                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16021
                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 16021
LENGTH: 77994
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SOFTWARE: FASEUSQ for Windows Version
SEQ ID NO 12517
LENGTH: 77994
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                                                                                                              Matches
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
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-09-949-016-12517
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT FILING DATE: 2000-04-14
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192; Conserv
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                                      CCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGATTCACTTGAGGTCAGGAGTTCG
                                                                       CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG
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Conservative
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                                                                                                          Score 148.8; DB 3; Pred. No. 1.4e-33; 0; Mismatches 72;
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RESULT 25
US-09-949-016-13461/c
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US-09-949-016-13460/c
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version SEQ ID NO 13460
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Patent No. 6812339
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human
-09-949-016-13460
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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                                                                                            GTCTCAAAAACAACAACAAAAAAAACAAA 343
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                                                                       GTCTCAAAAAAAAAAAAAAAAAAAA 6382
                                                                                                                                           TGAACCCAGGAGGCAGAGGTTGCAGTGAGCACTCCAACCTGGGCAACAGAGTGAGACTCT 6409
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OF DETECTION AND
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

Sequence 13461, Application US/09949016 Patent No. 6812339

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RESULT 26
U$-09-949-016-152016
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Best Local S
Matches 200
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 152016
                                         Query Match
Best Local Similarity
Matches 213; Conserv
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APPLICANT: VENTER, J.
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Patent No. 6812339
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                                                                                                                     TYPE: DNA
ORGANISM: Human
-09-949-016-152016
                                                                                                                                                                                                                                                                                                                                         APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
PILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
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ORGANISM: Human
-09-949-016-13461
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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PRIOR FILING DATE: 2000-10-03
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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84 CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG
                                       213; Conservative
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                                                            37.0%;
75.0%;
                                     Score 148; DB 3;
Pred. No. 3.4e-34;
1; Mismatches 61
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Pred. No. 6.4e-34;
1; Mismatches 60;
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                                       61;
                                                                             Length 601;
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RESULT 28
US-09-949-002-2954/c
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US-09-949-002-2953
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US-09-949-002-2953/c
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Sequence 2954, Application US/09949002
PATENT NO. 6900016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, N
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2953
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Patent No. 6900016
GENERAL INFORMATION:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, N
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
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les 176; Conserv
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Pred. No. 3.9e-34;
0; Mismatches 47
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METHODS OF DETECTION

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US-09-949-002-4465/c
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TYPE: DNA
ORGANISM: Human
0-09-949-002-2954
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: PASTSEQ for Windows Version 4.0
BBQ ID NO 4465
LENGTH: 601
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Best Local !
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, M
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
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Best Local Similarity
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Patent No. 6900016
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CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR PILING DATE: 2000-09-08
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
09-949-002-4465
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                                                                     TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
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                                                                                                                                             TCGAGACCATCCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                               ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTCGGCGGATCACCTGAGGTCAAGAGA 140
                                                  TGGGCATGGTGGCACACTTGTAGTCCCAGCTACTCAGGAGGCTGAGGCATGAGAATTG
                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                           Score 147.8; DB 3
Pred. No. 3.9e-34;
0; Mismatches 47
                                                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                           47;
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US-09-949-002-650
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 650, App
Patent No. 690001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4466, Apparent No. 690001
Query Match
Best Local Similarity
Matches 176; Conserv
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Best Local
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CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                         APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, N
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION UNUMERS: US/09/949,002
CURRENT FILING DATE: 2000-01-28
                                                                                                                                                                   NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSEQ for Windo
                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/231,401 PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FastSEQ for Windows Version
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                                                                                                              LENGTH: 60595
TYPE: DNA
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TYPE: DNA
                                                                                               ORGANISM: Human
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       Conservative
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                      37.0%;
78.9%;
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     Score 147.8; DB 3; Pred. No. 2.5e-33; 0; Mismatches 47;
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Pred. No. 3.
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         Indels
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ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140

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PRIOR APPLICATION NUMBER: 2000-01-28
PRIOR PLING DATE: 2000-01-28
PRIOR FLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: PRESEQ for Windows Version 4.0
SEQ ID NO 706
LENGTH: 60595
TYPE: DNA
ORGANISM: Human
US-09-949-002-706
Sequence 13849, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
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Best Local Similarity
Matches 176; Conserv
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Patent No. 6900016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, N
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
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2.5e-33;
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                                                                             US-09-949-016-13850
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US-09-949-016-13850
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; LOCATION: (1)...(86945)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-13849
                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 13850
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LENGTH: 86945
   Best Local Similarity
Matches 208; Conserv
                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6812339
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Best Local Similarity
                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-9-08
PRIOR FILING DATE: 2000-9-08
PRIOR FILING DATE: 2000-9-08
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(86945)
OTHER INFORMATION: n =
                                                                                                                                                          FEATURE:
                                                                                                                                                                      ORGANISM: Human
                                                                                                                                                                                            TYPE: DNA
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73.5%;
                 37.0%;
                                                                                               A, T, C
Score 147.8; DB
Pred. No. 2.9e-33
1; Mismatches 51
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Pred. No. 2.9e
1; Mismatches
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                                     DB 3;
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                                   Length 86945;
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Conservative

Indels

16;

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RESULT 35
US-09-949-016-13851, Appl
; Sequence 13851, Appl
; Sequence 13851, Appl
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NAME/KEY: misc feature
LOCATION: (1)...(86945)

OTHER INFORMATION: n = A,T,C or
US-09-949-016-13851
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version SEQ ID NO 13851 LENGTH: 86945
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human
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  GAGTGAGACKCCGTCTCAAAAACAACAACAAAAAACAAAAAA
                                           CTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTGTGCCATTGTACTCCAGCCTGGGCAACA
                                                                                   TGAGATCGCAGAGTGAGCCGAAATCACAGAT ------CACAGAGTGAGCA
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73.5%;
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; FEATURE:
, NAME/KEY: misc feature
; LOCATION: (1)...(86945)
; OTHER INFORMATION: n = A,T,C
US-09-949-016-13852
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241.755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0
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RESULT 37
US-09-949-016-13853
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Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 13852
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Best Local Similarity
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73.5%;
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: U\$/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/21,755

PRIOR TILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

ASSOCIATED OF DETECTION

DETECTION AND USES THEREOF

Sequence 13853, Application US/09949016 Patent No. 6812339

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RESULT 38
U$-09-949-016-13854
                                                  Query Match
Best Local Similarity
Matches 208; Conserv
                                                                                                                     LENGTH: 86945

TYPE: DNA
ORGANISM: Human
ORGANISM: Human
PEATURE: misc feature
LOCATION: (1)...(86945)
OTHER INFORMATION: n = A,T,C or G
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SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 13853
LENGTH: 86945
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                       SEQ ID NO 13854
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Best Local Similarity
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LOCATION: (1)...(86945)
OTHER INFORMATION: n = A,T,C or
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                 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
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                                                  Score 147.8; DB 3
Pred. No. 2.9e-33;
1; Mismatches 58
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Pred. No. 2.9e-33;
1; Mismatches 58
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                                                                              Length 86945;
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US-09-949-016-13855
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR TILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 208; Conserv
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LENGTH: 86945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(86945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                                                                   TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                  TTGAGACCAGCCTGGCCAACATGGTAAAACCCCTGTCTACTAAAAAATACAAAAATGAGC
                                                                                                                                                                                                                                                                                      ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
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                                       CTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTGTGCCCATTGTACTCCAGCCTGGGCAACA
                                                                         TGAGATCGCAGAGTGAGCCGAAATCACAGAT------CACAGAGTGAGCA 304
                                                                                                              TGGGCGTGGTGCTGCACCTATAATCCTAGCTACTCAGGAGGCTGAGGTTGCAGTGAAC
                                                                                                                                                                                                                                                         ATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGAGGATTACTTGAGGTCAGGAGT
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73.5%;
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                                                                                                                                                                                                                                                                                                                           Score 147.8; DB 3
Pred. No. 2.9e-33;
1; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                             DB 3;
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASKSEQ for Windows Version 4.0
SEQ ID NO 13857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-09-949-016-13856
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Patent No. 6812339
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ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(86945)
OTHER INFORMATION: n = A,T,C o
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Best Local Similarity
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                                                                                                                                                                                                                                                                                           Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J.
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                                                                                                                                                                                                                         TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS FILE REFERENCE: CLOO1307
                                                                                                                                                                                                                                                                                                                                                        Sequence 13857,
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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TITLE OF INVENTION: POLYMORPHIENS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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73.5%;
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Pred. No. 2.9e-33;
1; Mismatches 58
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT ETLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PRICATION NUMBER: 60/231,498
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; LOCATION: (1)...(86945)
; OTHER INFORMATION: n =
US-09-949-016-13857
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US-09-949-016-13858
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Best Local Similarity
Matches 208; Conserv
                                                                                                                                              Query Match
Best Local
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SEQ ID NO 13858
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                                                                                                                             Matches 208;
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                                                                                                                                                                                                                  ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(86945)
OTHER INFORMATION: n = A
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                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                Local Similarity
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141 TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATATACAAAAAATAGC
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                                                                           ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
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Pred. No. 2.5
                                                                                                                             Score 147.8; DB 3
Pred. No. 2.9e-33;
L; Mismatches 58
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
SOFTWARE: FRABLSEQ for Windows Version 4.0
SEQ ID NO 14022:
TYPER: DAYS
TYPER: DAYS
TYPER: DAYS
                                                                                                                                                            RESULT 44
US-09-949-016-12819
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U$-09-949-016-14022
          GENERAL INFORMATION:
APPLICANT: VENTER, J.
TITLE OF INVENTION: PO
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Best Local Similarity 75.4
Matches 199; Conservative
                                                                                                          Sequence 12819, Ap
Patent No. 6812339
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ORGANISM: Human
-09-949-016-14022
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE; CL001307
                                                                                                                                                                                                                                                               1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 AGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG 143
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                                                                                                                                                                                                                                                                                                              AAACAACAACAAAAAACAAAAAAA 347
                                                                                                                                                                                                                                                                                                                                                                                                            GATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACGAAAAACAAAAAACAGCACAA 1218
                                                                                                                                                                                                                                                                                                                                                               GATCACAGCCCTGCACTCCAGCCTGGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGACCAGCCTGGCCCACATGGTGAAACCCCCGTCTCTACTAAAAATACAAAAATTAGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGTGAGACKCCGTCTCAAAAACAACAACAAAAAAAAACAAAAAA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGGAGGCAGAGGTTGCAGCTGAGATTGTGCCATTGTACTCCAGCCTGGGCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAGATCGCAGAGTGAGCCGAAATCACAGAT------CACAGAGTGAGCA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGGCGTGGTGTGCACCTATAATCCTAGCTACTCAGGAGGCTGAGGTTGCAGTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGAGACCAGCCTGGCCAACATGGTAAAACCCTGTCTCTACTAAAAATACAAAAAATGAGC 25122
                                                                                                                                    Application US/09949016
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J. Craig et al.
POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.9%;
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Pred. No. 1.4e-
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , DB 3;
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Best Local Similarity Matches 199; Conserv

Conservative

36.9%; 75.4%;

Score 147.6; DB 5; Pred. No. 1.5e-33; 1; Mismatches 55;

DB 5;

Length 11820;

Indels

9;

Gaps

1;

Query Match

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US-09-936-271C-56
                                                                                              CURRENT APPLICATION NUMBER: US/09/936,271C
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: PCT/CA00/00258
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/124,260
PRIOR FILING DATE: 1999-03-11
PRIOR PPLICATION NUMBER: US 60/127,386
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-07-21
PRIOR PILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 97
SOPTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-936-271C-56
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; ORGANISM: Human
US-09-949-016-12819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                           SEQ ID NO 56
LENGTH: 11820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 56, Appli
Patent No. 7022497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version SEQ ID NO 12819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yousef, George M.
APPLICANT: Diamandis, Eleftherios
TITLE OF INVENTION: No. 7022497el 1
                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: MTS3USA
                TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGACCATCCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09936271C
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                                                                                                                                                                                                                                                                                                                                                                                            7022497el Human Kallikrein-Like Genes
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Pred. No. 1.4e-33;
1; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55;
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; LENGTH: 26967
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12926
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US-09-949-016-12926/c
; Sequence 12926, Application US/09949016
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| CURRENT FILING DATE: 2000-04-14
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR FILING DATE: 2000-10-20
| PRIOR APPLICATION NUMBER: 60/237,768
| PRIOR FILING DATE: 2000-10-03
| PRIOR PPLICATION NUMBER: 60/231,498
| PRIOR FILING DATE: 2000-09-08
RESULT 47
US-09-949-016-15831/c
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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Best Local Similarity
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                         47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACATGGTGGCACGTGCCTGTAATCCCAGGTACTCAAGAGGTGGAGGTTGCAGTGAGCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGTAATCCCGGCACTTTGGGAAGCCAAGGCAGGCAGGTTGCTTGAGGCCAGGAGTTCA 2765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATCACAGCCCTGCACTCCAGCCTGGGTGA------CAGAGCGAGACTCCATCTCAA 2936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTGAACCCAGGAGGTGGAGGCTGCAGTGAGCCGAGATCATGCCACTGCACTCCAGCCTG 1696:
                                                                                                                                                                                                                                                                     TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGA-----
                                                                                                                                                                                                                                                                                                                                                                             TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAAGACCAGCCTGGGAAACATGGTGAAACCCCCATCTCTACTAAAAATACAAAAATTAGC
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                                                                                                                                                             -GTGAGCAGAGTGAGACKCCGTCTCAAAAACAACAACAAAAAAACAAAAAAAACCATAA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 147.4; DB 3;
Pred. No. 2.4e-33;
1; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASSOCIATED OF DETECTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16792
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US-09-949-016-16792
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
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SEQ ID NO 15831
LENGTH: 35104
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16792, Application US/09949016 Patent No. 6812339
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Best Local :
                                                                                SOFTWARE: FastSEQ for Windows Version SEQ ID NO 16792
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TITLE OF INVENTION: POLYMORPHIENS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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Pred. No. 2.6e
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHIENS IN KNOWN GENES ASSOCIATED
FILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-949-016-17565
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|Best Local Similarity 73.1
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TYPE: DNA
ORGANISM: Human
9-09-949-016-17565
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Matches 225;
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CTTGAACCCAGGAGGTGGAGGGGAGCCGGACTCAGCGGACAACAGAGGCGAGACTCCATC 77196
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                                   TGAGATCGCAGAGTGAGCCGAAATCACAGATCA-CAGAGTGAGCAGAGTGAGACKCCGTC
                                                                                                      TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
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                                                                               TGGGTGTGGTGCACACCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAACTG
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Pred. No. 4.3e-33;
1; Mismatches 72;
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Pred. No. 3.1e-33;
1; Mismatches 87;
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; ORGANISM: Human
; FEATURE;
; NAME/KEY: misc_feature
; LOCATION: (1)...(301828)
; OTHER INFORMATION: n = A,T,C
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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LENGTH: 301828
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: CL001307
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Local Similarity 72.6%;
69312
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                           AGACKCCGTCTCAAAAACAACAACAAAAAACAAAAAAACCATAAGACA
                                                                       GAACCCTGGAGACGGAGGTTGCAGTGAGCTGAGATCACGCCCAGCCTGGACAACAGAGCA
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 GATCGCAG------AGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTG
                                                                                                                                                   GTGTGGTGGCAGGCACCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGAGAATGGCTT
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Pred. No. 7.2e-33;
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OF DETECTION AND
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Search completed: July 17, 2006, 20:41:42 Job time: 170 secs

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Maximum
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Perfect score:
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1: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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6: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
9: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
10: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
12: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
13: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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US-10-741-601-17658
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US-10-741-600-36121
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RESULT 1

US-10-741-601-5648/c

Sequence 5648, Application US/10741601

Sequence 100 No. US20040166519A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHIS

TITLE OF INVENTION: STENOSIS, METHODS
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Michele et al.
GENETIC POLYMORPHISMS ASSOCIATED WITH
STENOSIS, METHODS OF DETECTION AND USES THEREOF
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US-10-956-157-8256
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Sequence 11, Appl
Sequence 4, Appli
Sequence 166, App
Sequence 580582,
Sequence 741359,
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Sequence 1277, Ap
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Sequence 742, App
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Sequence 3751, App
Sequence 4, Appl1
Sequence 4, Appl1
Sequence 11870, Ap
Sequence 11870, Ap
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Sequence 49, Appl
Sequence 442, App
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Sequence 1113, Ap
Sequence 1788, Ap
Sequence 1798, Ap
Sequence 98, Appl
Sequence 4513, Ap
Sequence 229704,
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RESULT 2
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                                            NAME/KEY: misc_feature; LOCATION: (1)...(36805); OTHER INFORMATION: n = US-10-741-600-17657
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                                                                                                                                               GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DET
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEO ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17657
LENGTH: 38685
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CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5648
LENGTH: 36805
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OTHER INFORMATION: n =
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2; Mismatches 1;
 Score 397.2; DB 9;
Pred. No. 2.2e-111;
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                                                            or insertion/deletion polymorphism (see Tables
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SEQ ID NO 5649

LENGTH: 75729

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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US-10-741-601-5649/c
                                                                                                                                                                                                                                                                                          Query Match
Best Local Simi
Matches 397;
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APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT PILLING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FRACTSEQ for Windows Version 4.0
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Publication No. US20040166519A1
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LOCATION: (1)...(75729)
OTHER INFORMATION: n = A,T,C
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                               CTAAAAATACAAAAAATAGCTGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGG
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Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS AS:
TITLE OF INVENTION: MYOCARDIAL INFARCTION,
FILE REFERENCE: CL001499
CURRENT APPLICATION UNMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
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RESULT 5
US-10-741-601-13924/c
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; LOCATION: (1)...(75729)
; OTHER INFORMATION: n =
US-10-741-600-17658
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US-10-741-600-17658/c
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LENGTH: 75729
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ORGANISM: Homo sapiens
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GENETIC POLYMORPHISMS ASSOCIATED WITH
MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
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Pred. No. 3e-111;
2; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14097
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-741-601-14097
                                                       RESULT 6
US-10-741-601-14097/c
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APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13924
TENOTH: 201
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Matches
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Publication No. US20040166519A1
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APPLICANT: CARGIIL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500
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TGGTGGCACACACCTGTAGTC 227
                                  CCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCA
                                                       CCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCA
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nilarity 99.0%;
Conservative
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Pred. No. 5.9e-51;
1; Mismatches 1
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Pred. No. 5.9e-51;
1; Mismatches 1
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Sequence 35944, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECT
FILE REFERENCE: CL001499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 35944

LENCTH: 201
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US-10-741-600-35944/c
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CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
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TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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GTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGA
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GENETIC POLYMORPHISMS ASSOCIATED WITH
MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES
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Pred. No. 5.9e-51;
1; Mismatches 1
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Pred. No. 5.9e-51;
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RESULT 9
US-10-741-601-13993/c
(Sequence 13993, Application US/10741601

Publication No. US20040166519A1

Publication No. US20040166519A1

PUBLICANT: CARGILL, Michele et al.

PTITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001500

CURRENT APPLICATION NUMBER: US/10/741,601

CURRENT PILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 26415

SOFTWARE: FABSESEQ FOR WINDOWS Version 4.0

FENCHUS. 2013-93.
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                                                                                                                       GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1500

CURRENT APPLICATION NUMBER: US/10/741,601

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 26415

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14060

LENGTH: 201
   Query Match
Best Local Similarity
Matches 196; Conserv
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Best Local Similarity
                                                                    TYPE: DNA ORGANISM: Homo sapiens -10-741-601-14060
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ORGANISM: Homo sapiens
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Pred. No. 2.1e
2; Mismatches
Score 197.2; DB 8;
Pred. No. 2.1e-50;
2; Mismatches 0;
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Sequence 3604, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECT

PILE REFERENCE: CL001499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 36084
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Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS AS
TITLE OF INVENTION: MYOCARDIAL INFARCTION,
FILE REFERENCE: CLOO1499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOPTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 36017
LENGTH: 201
TYPE: DNA
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US-10-741-600-36084/c
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GENETIC POLYMORPHISMS ASSOCIATED
MYOCARDIAL INFARCTION, METHODS C
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Pred. No. 2.1e-50;
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US-10-741-600-36084

DB 9;

Length

TYPE: DNA
ORGANISM: Homo sapiens

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RESULT 13

US-10-741-601-13992/c

Sequence 13992, Application US/10741601

Publication No. US20040166519A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: INVENTION: GENETIC POLYMORPHISMS ASS
TITLE OF INVENTION: STENOSIS, METHODS OF DET

FILE REFERENCE: CL001500

CURRENT APPLICATION NUMBER: US/10/741,601

CURRENT APPLICATION NUMBER: US/10/741,601

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 26415

SEQ ID NO 13992

LENGTH: 201

TYPE: DNA

ORGANISM: Homo sapiens
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US-10-741-601-14059/c
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     Sequence 14059, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: STENOSIS, METHODS
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Best Local Similarity
Matches 196; Conserva
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Michele et al.
GENETIC POLYMORPHISMS ASSOCIATED WITH
STENOSIS, METHODS OF DETECTION AND USES THEREOF
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Pred. No. 1.3e-46;
0; Mismatches 1
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Pred. No. 2.1e-50;
2; Mismatches 0
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; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOPTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14559
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-14059
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DET
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36016
LENGTH: 201
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Best Local Similarity
Matches 186; Conserv
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Best Local Similarity
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ORGANISM: Homo sapiens
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Pred. No. 1.3e-46;
0; Mismatches 1
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Pred. No. 1.3e-46;
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US-09-764-891-6505
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Best Local S
Matches 201
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING.DATE: 2003-12-22
NUMBER: FBSUSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                        Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6505
LENGTH: 16163.
TYPE: DNA
ORGANISM: Homo sapiens
9-09-764-891-6505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6505, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
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TYPE: DNA
ORGANISM: Homo sapiens
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CCAGCTGGGTGTGGTACACGCTTGTAATCCCAGCTACTCTGGAGGCGGAGGTTGCAG
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Pred. No. 1.2e-37;
0; Mismatches 71;
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Pred. No. 1.3e-46;
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RESULT 19
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; ORGANISM: Homo sapiens
US-10-091-414-270
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US-10-091-414-270
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GENERAL INFORMATION:
APPLICANT: MORTIS, David
APPLICANT: Engelhard, Eric
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
FILE REFERENCE: A-71171/ENS/DCF
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
                                                                                                                                                    Sequence 16, Application US/09997722
Publication No. US20040072154A1
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LENGTH: 16163
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Publication No. US20030224461A1
GENERAL INFORMATION:
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PALIGC1
CURRENT APPLICATION NUMBER: US/10/091,414
CURRENT FILING DATE: 2002-03-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 392
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Local Similarity 73.9%;
les 201; Conservation
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PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-03 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTMARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 96593

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; | ORGANISM: Homo sapien
US-10-301-480-603905
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TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 603905
LENGTH: 997
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Best Local Similarity
Matches 216; Conserv
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Best Local Similarity
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                                                                                                             TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
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CAAAAACAACAACAAAAAAACA 341
                               TGAGATTG----
                                                           TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                             TGGGCATGGTGGCAGGGCCTGTAATCCCCAGCTACTCAGGAGGCGGAGGTTGCAGTGAGC
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Pred. No. 4.7e-38;
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LENGTH: 63

635

ORGANISM: Homo sapien

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APPLICANT: Wand, David G.
TITLE OF INVENTION: Identifiction and Mapping of
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR PRICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER: OF SEQ ID NOS: 1226618
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 577516
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; ORGANISM: Homo sapien
US-10-301-480-1217314
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Best Local Similarity
Matches 205; Conserv
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 1217314
LENGTH: 997
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Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
                                                                                                                                                                                                                                                                                Sequence 577516, Application US/10301480 Publication No. US20060057564A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/301,480 CURRENT FILING DATE: -2002-11-21 PRIOR APPLICATION NUMBER: US 10/215,598 PRIOR FILING DATE: 2002-08-09 PRIOR APPLICATION NUMBER: US 60/311,695 PRIOR FILING DATE: 2001-08-10 PRIOR FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCAGGCGGATTACCTGAGGTCTGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            САЛАЛАСЛАСЛАСЛАЛАЛАЛСА 341
                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAGATCGCAGAGTGAGCCGGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGGCATGGTGGCAGGGCCTGTAATCCCCAGCTACTCAGGAGGCCGGAGGTTGCAGTGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAGATTG-----TGCCACTGCACTCCAGCCTGGGTGACAAGAGCAAAACACTGTCT 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 158.2; DB 1
Pred. No. 4.7e-38;
0; Mismatches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12;
                                                                                                                                                                                                                                             of Single
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US-10-301-480-1190925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATI: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: F8stSEQ for Windows Version 4.0
SEQ ID NO 1190925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1190925, Application UPublication No. US20060057564A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 206
                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo mapien
-10-301-480-1190925
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 635
                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                         206;
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                                                                                                                                                                                                                        312
                                                                                                                                                                                                                                          141 TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                                                    252 ACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGGATAACCTGAGGTCAGGAGT 311
                 484
                                                 321
                                                                                  432
                                                                                                                    261
                                                                                                                                                                              201 TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGC
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                                                                                                                                                                                                                                                                                                                      81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206;
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                                            CAAAAACAACAACAAAAAACAAAAAAA 347
                                                                                                                TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                                                TGGGCATGATGGCGGGTACCTGTAATCCCAGCTACTCGGGAGGCGGAGGTTGCGGTGAGC
                                                                                                                                                                                                                   TCAAGACCAGCCTGGCCAAAATGGTGAAACCCCCATCTCTACTAAAAATACAAAAATTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGAGATCG-----TGCCATTGCACCCCAGCCTGGGCAACAAGAGCGAAACTCTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAAGACCAGCCTGGCCAAAAATGGTGAAAACCCCCATCTCTACTAAAAATACAAAAATTAGC 371
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                                                                                  -TGCCATTGCACCCCAGCCTGGGCAACAAGAGCGAAACTCTGTCT
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                                                                                                                                                                                                                                                                                                                                                       Score 157.4; DB 12;
Pred. No. 6.9e-38;
1; Mismatches 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                      52; Indels
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US-10-027-632-98771/c
; Sequence 98771, Application US/10027632
; Publication No. US20030204075A9
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GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/218,006
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; LENGTH: 1963
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-98771
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR PPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,358
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 24
US-10-027-632-98771/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 98771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 98771, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1999-08-09 NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                           CCGGAGTGGTGGTGGCCCTGTAGTCCCAACTACTCGGGAGGCGGAGGTTGCAGTGAGC 284
CAACAACAATAACAAAAAAAAAACAAGTGCAAGGTCTTGCCTTTGAGTTGGGGTCAGA
                                               СААВААСЛАСААСААЛАЛАЛАЛАЛАЛАССАТЛАНGACATTGTCCATCTGCGGTTCCCAGA 379
                                                                                                             CGAGACCACGCCTTTGCACTCCAGCCTGGGCGA-----CAGAGCGAGACTCTGTCT
                                                                                                                                                                                                                                                                              TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                                                                                                                                                                                                  ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                                                                                                                                                                                                                                         TCGAGACCAGCCTGGCCAAAATGGTGAAACCCCCGTCTCTACTAAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGCCTATAATCCCAGCACTTTGGAAGGCCAAGGTGGGCGGATCACTTGAGGCCAGGAAT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 155.4; DB 6; Pred. No. 4.5e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72;
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174
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; LENGTH: 1963
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-98771
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US-10-087-192-760/c
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Publication No. US20
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 38.5
Best Local Similarity 72.6
Matches 217; Conservative
Query Match
Best Local Similarity
Matches 217; Conserv
                                                                                                                    SOFTWARE: FastSEQ for Windows Version SEQ ID NO 760 LENGTH: 31898
                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                     APPLICANT: MOTTIS, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
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PRIOR
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                                                                       ORGANISM: Homo sapiens
-10-087-192-760
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OR FILING DATE: 2000-04-20
OR APPLICATION NUMBER: US 60/193,483
OR FILING DATE: 2000-03-29
OR APPLICATION NUMBER: US 60/185,218
OR FILING DATE: 2000-02-24
OR APPLICATION NUMBER: US 60/167,363
OR FILING DATE: 1999-11-23
OR APPLICATION NUMBER: US 60/156,358
OR FILING DATE: 1999-09-28
OR APPLICATION NUMBER: US 60/146,002
OR APPLICATION NUMBER: US 60/146,002
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      Conservative
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Pred. No. 4.5e-37;
1; Mismatches 72
     Score 155.4; DB 6;
Pred. No. 1.4e-36;
1; Mismatches 72;
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human G
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/260,786
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Sequence 532789, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
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SEQ ID NO 532789
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PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
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ORGANISM: Homo
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Pred. No. 4.3e-37;
2; Mismatches 89;
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RESULT 29
US-10-301-480-609460/c
US-10-301-480-609460, Application US/10301480
; Sequence 609460, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
    APPLICANT: Wang, David G.
    TITLE OF INVENTION: In the Human Genome
; FILE REFERENCE: 108827.137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U$-09-925-065A-532789/c
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PRIOR PILING DATE: 2000-10-24
PRIOR PPLICATION NUMBER: US 60/252,147
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-11-6
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
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ORGANISM: Homo sapiens
-09-925-065A-532789
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08
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Pred. No. 4.3e-37;
2; Mismatches 89;
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FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOPTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1222869
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                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1222869
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US-10-301-480-1222869/c
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US-10-301-480-609460
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
                                                                      Matches
                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1222869, Application US/10301480 Publication No. US20060057564A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 609460
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                                                                 Local Similarity hes 218; Conserv
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AGAAACAGTGTGGCAGGCCGGGTGCGGTGCACACCTGTAATCCCAGCACTTTGGGAG
                    AGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCTGTAATCCCCAGCACTTCGGGAG 107
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                                                                    Conservative
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                                                                                   38.4%;
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                                                                  Pred. No. 1.2e-36;
L; Mismatches 90
                                                                                                      Score 153.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 153.6; DB 12;
Pred. No. 1.2e-36;
1; Mismatches 90;
                                                                                                    DB 12;
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                                                                  Indels
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377
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FEATURE:
NAME/KEY: misc feature
LOCATION: (1): ... (415117)
OTHER INFORMATION: n = A,T,C
US-10-995-561-13274
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US-10-995-561-13274/c
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CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 13274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13274, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOUISS9
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TYPE: DNA
                                                                                                                                           228332
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                                                                                                                                                                                                                                                                                                                       99
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                                                                                                                                                                                                                                                                                                                                                                                                                               224;
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                                                                  CCAGCTACTCAGGAGGCTGAGGCAGGAGAATCTCTTGAACCTGGGAGGCGGAGGTTGCAC
AGAAAGTAAATAAATTTATTCAT 228189
                               ACAAAAAACCATAAGACATTGTCCAT 365
                                                                                                    CGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAAAAAACAACAACAAAAA
                                                                                                                                         CCTGTAATCCCACTTACTCGGGAGGCAAAGGTTGCAATGAGCCCAGATTGCACCACTGCA 228273
                                                                                                                                                                            CCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAGATCGCAGAGTGAGC
                                                                                                                                                                                                                 ACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCCAGTCGTGGTGGCACACA
                                                                                                                                                                                                                                                 CTTTGAGAGGCCGAGGTGGGTGGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 415117;
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GENERAL INFURFACION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identifiction and Mapping of

TITLE OF INVENTION: In the Human Genome

FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 10/215,598

PRIOR PILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 598906

LENGTH: 984
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1212315
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US-10-301-480-598906
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 33
US-10-301-480-1212315
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                                                        SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1212315
LENGTH: 984
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    Sequence 1212315, Application US/10301480 Publication No. US20060057564A1
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Best Local
                                                                                                                 CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
                                                                                                                                                                                                                                                                       APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping
TITLE OF INVENTION: in the Human Genome
                                                                                                                                                                                                                                                         FILE REFERENCE: 108827.137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCTGTCTCAAAAAAAAAAAAAAATTAGCTGGGCATAGT
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Pred. No. 1.9e-36;
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RESULT 35
US-09-567-768A-314/c
; Sequence 314, Application US/09967768A
; Patent No. US20020150877A1
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SEQ ID NO 7647
LENGTH: 4388
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-7647
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US-09-764-891-7647/c
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Best Local S
Matches 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Sir
hes 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                        TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGC
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76.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 152.4; DB 3;
Pred. No. 5.3e-36;
1; Mismatches 52;
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Pred. No. 1.9e-36;
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APPLICANT: Munger, William B.
TITLE OF INVENTION: Identifying Drugs for and Di.
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5029-01US
CURRENT APPLICATION NUMBER: US/09/960,706
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/223,323
PRIOR APPLICATION NUMBER: 60/223,323
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION UMBER: 09/873,319
PRIOR FILING DATE: 2001-06-05
                                                                   ; OTHER INFORMATION: Genbank Accession No. US-09-960-706-969
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                                                                                                                                                        NUMBER OF SEQ ID NOS: 1124
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 969
LENGTH: 174424
TYPE: num
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CURRENT APPLICATION NUMBER: US/09/967,768A

CURRENT FILING DATE: 2001-09-28

PRIOR APPLICATION NUMBER: US/60/236,109

PRIOR APPLICATION NUMBER: US/60/236,034

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US/60/236,034

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US/60/236,111

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US/60/236,111

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 969, Application US/09960706 Publication No. US20030134280A1 GENERAL INFORMATION:
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.0 SEQ ID NO 314
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APPLICANT: Augustus
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TITLE OF INVENTION: Cancer Gene Determination
TITLE OF INVENTION: Sets
                                                                                                          TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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  38.0%;
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Score 152; DB 3; Pred. No. 3e-35;
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Pred. No. 3e-35;
0; Mismatches
                                                                                     US20030134280A1 U52112
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                  Length 174424
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RESULT 37
US-10-843-641A-6459/c
, Sequence 6459, Application US/10843641A
, Publication No. US20050064454A1
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                                                                                                                                                                                              Query Match
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PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US/09/954,531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Avalon Pharmaceuticals, Inc.
TITLE OF INVENTION: Cancer Gene Determination
TITLE OF INVENTION: Signature Gene Sets
                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 689290-189
                                                                                                                                                                                                                                         10-843-641A-6459
                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                   TYPE: DNA
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OR FILING DATE: 2001-09-18
OR APPLICATION NUMBER: US/09/954,456
OR FILING DATE: 2001-09-25
OR APPLICATION NUMBER: US/09/962,436
OR FILING DATE: 2001-09-25
OR APPLICATION NUMBER: US/09/962,832
OR APPLICATION NUMBER: US/09/962,832
OR FILING DATE: 2001-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR APPLICATION NUMBER: US/09/964,824
OR FILING DATE: 2001-09-27
OR APPLICATION NUMBER: US/09/967,768
OR FILING DATE: 2001-09-28
OR APPLICATION NUMBER: US/09/968,007
OR FILING DATE: 2001-10-02
OR APPLICATION NUMBER: US/09/969,347
OR FILING DATE: 2001-10-02
OR FILING DATE: 2001-10-02
                                                                   48438 TCCTCAGGTGTCTGGTGATCCTTGGTTGTCTTCTCATATTTAAGAATGGGGCAGGCTGGG
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66 CATGACACTGGCTGAATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCA
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                                                                                                         TACTCAGCCATGTGCTGGGCCATGGGAACCCCAAATATTAATAAGACATTGTCAGGCCAGG
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                                                                                                                                                    Score 152; DB 1
Pred. No. 3e-35;
0; Mismatches
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RESULT 39 US-10-756-149-2215/c

Sequence 2215, Application US/10756149
Publication No. US20050181375A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER

FILE REFERENCE: file

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Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators FILE REFERENCE: 05882.0193.NPUS01 CURRENT APPLICATION NUMBER: US/10/723,860 CURRENT FILING DATE: 2003.11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
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                                 GAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGC 303
                                                                                                                                                               CCTGAGGTCAAGAGCAAGTCCATCCTGGCCAACATGGTGAAACCCCTGTTTGTACTAAA 48264
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Pred. No. 3.1e-35;
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CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: PACENTIN VERSION 3.2
SEQ ID NO 2215
SEQ ID NO 2215
LENGTH: 181343
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-756-149-2215
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US-09-925-065A-45529
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PRIOR FILING DATE: 2000-11-20
PRIOR PELICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
                                                                                                                                Query Match 37.9
Best Local Similarity 74.2
Matches 224; Conservative
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APPLICANT: Wand, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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Best Local Similarity
Matches 214; Conserv
                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
-09-925-065A-45529
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 45529
                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 957086
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PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                         ENGTH: 599
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143 GAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTG
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                                          GCCTGTAATCCCAGCACTTTGGGAGGCTAAGGTGGGCGGATCACCTGAGGTCAGGAGTTC
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                                                                                                                              Score 151.6; DB 4;
Pred. No. 4.2e-36;
2; Mismatches 56;
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Pred. No. 3.1e-35;
0; Mismatches 80
                                                                                                                                56; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILLING DATE: 2000-11-20
PRIOR PELICATION NUMBER: US 60/250,092
PRIOR FILLING DATE: 2000-11-30
PRIOR PELICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILLING DATE: 2001-01-16
PRIOR PELICATION NUMBER: US 60/289,846
PRIOR FILLING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 45529, Application US/09925065A Publication No. US20050228172A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 37.9%;
Best Local Similarity 74.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 45529
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 599
TYPE: DNA
ORGANISM: Homo mapiens
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                                                                                                                                               GACATGGTGGCACGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGAATCACTTGA 181
                                                                                                                                                                         GGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCC----GGAGATTGCAGTGA
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ACCCRGGAGGCAGAGGTTGCAGTGAGCCAAGATCACGCCACTGCACTTCAGCCTGGGTGA 241
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Pred. No. 4.2e-36;
2; Mismatches 56;
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RESULT 42

US-10-301-480-146767

US-10-301-480-146767, Application US/10301480

Sequence 146767, Application US/10301480

publication No. US20060057564A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identifiction and Mapping of TITLE OF INVENTION: in the Human Genome FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 10/215,598

PRIOR FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10
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US-10-301-480-760176
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US-10-301-480-146767
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 146767
LENGTH: 599
                                                                                                                                                                                                         Sequence 760176, Application US/10301480 publication No. US20060057564A1 GENERAL INFORMATION:
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Best Local
APPLICANT: Wang, David G.

TITLE OF INVENTION: In the Human Genome
TITLE OF INVENTION: IN the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT APPLICATION NUMBER: US/10/215,598
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
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Pred. No. 4.2e-36;
2; Mismatches 56
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; TYPE: DNA; Homo sapien; ORGANISM: Homo sapien US-10-301-480-760176
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                                                                                                                          , OTHER INFORMATION: Genbank Accession No. AC005082 US-10-450-826-93
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Best Local Simi
Matches 224;
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LENGTH: 599
                                                    Query Match
Best Local Similarity
Matches 229; Conser
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Publication No. US20040101818A1
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APPLICANT: Axe
APPLICANT: Coo
                                                                                                                                                                                                                            SEQ ID NO 93
                                                                                                                                                                                                                                                                                                    APPLICANT: Houghton, Adam
APPLICANT: Mertz, Lawrence
TITLE OF INVENTION: Gene Expression Profiles Associated with
FILE REFERENCE: 044921-5039-WO
CURRENT APPLICATION NUMBER: US/10/450,826
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 60/255,882
PRIOR FILING DATE: 2000-12-18
                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/285,691
PRIOR FILING DATE: 2001-04-24
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                            FEATURE:
                                                                                                                                                                                                         LENGTH: 169739
125892 GGTAAGAAAATCTTAGTTAAAGATCTAAAGTTTTGGCCAGGCACAGTGGCTAACGCCTGTA 125833
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                  GGAACCCAAATATTAATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCTGTA 89
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Eistein, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cook,
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                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jonathon
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70.98;
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                                                          Score 151.4; DB o;
Pred. No. 4.6e-35;
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Pred. No. 4.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56;
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                                                                                            Length 169739;
                                                               Indels
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                                                               Gaps
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RESULT 46
US-10-995-561-13489/c
; Sequence 13489, App
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US-10-331-053-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 211; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(133300)
OTHER INFORMATION: n = A,T,C
-10-331-053-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 70
LENGTH: 133300
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 70, Application US/10331053 Publication No. US20040197778A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and
FILE REFERENCE: 529452001100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/331,053
CURRENT FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                         TCAAAAACAACAACAAAAACAAAAAACCATA
                                                                                                                                                                                   CCGAGATCGCGTCACTGCACTCCAGCCTGGGCGA-----
                                                                                                                                                                                                                CTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTC
                                                                                                                                                                                                                                                                                            CTGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                   TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAA-TAG
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  Application US/10995561
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Pred. No. 5.6e-35;
1; Mismatches 51
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; Sequence 797, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins,
; FILE REFERENCE: PC008
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                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-797
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                                                                                                                                                                                                     SOFTWARE: Patentin Ver. SEQ ID NO 797
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Best Local Similarity
Matches 199; Conserv
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APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRU
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOUI559
CURRENT APPLICATION UNMER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
                                                                   Matches
                                                                                                     Query Match
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LENGTH: 195998
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                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/764,860
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM
NUMBER OF SEQ ID NOS: 1198
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NAME/KEY: misc_feature
LOCATION: (1)...(195998)
OTHER INFORMATION: n = A,T,C or G,
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ORGANISM: Homo sapiens
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                                                                 Local Similarity
les 224; Conser
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                   ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
ACGCCTGTAATGCTAGCACTTTGGGAĞGCCAAĞĞCGGAĞGATCACTTGAGGTCAGGAGT 2378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAAAACAACAACAAAAAA 339
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                                                                   Conservative
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                                                                                 37.7%;
                                                                Score 150.6; DB 3;
Pred. No. 4.2e-35;
1; Mismatches 95;
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Pred. No. 6.5e-35;
1; Mismatches 51;
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FILING DATE: 2000-07 APPLICATION NUMBER: FILING DATE: 2000-08 APPLICATION NUMBER: FILING DATE: 2000-07 APPLICATION NUMBER: FILING DATE: 2000-08 APPLICATION NUMBER: FILING DATE: 2000-08 APPLICATION NUMBER: FILING DATE: 2000-07 APPLICATION NUMBER: FILING DATE: 2000-07 APPLICATION NUMBER: FILING DATE: 2000-08 APPLICATION NUMBER: FILING DATE: 2000-07 APPLICATION NUMBER: FILING DATE: 2000-08	RESULT 48 RESULT 48 Sequence 797, Application US/10074 Publication No. US20030077704A1 GENERAL INFORMATION: APPLICANT: ROSEN et al. TITLE OF INVENTION: Nucleic Acids FILE REFERENCE: PC008C1 FILE REFERENCE: PC008C1 CURRENT APPLICATION NUMBER: US/10 CURRENT FILING DATE: 2002-02-14 PRIOR APPLICATION NUMBER: 60/179, PRIOR APPLICATION NUMBER: 60/179, PRIOR FILING DATE: 2000-01-31 PRIOR APPLICATION NUMBER: 60/180, PRIOR FILING DATE: 2000-02-04 PRIOR APPLICATION NUMBER: 60/214, PRIOR APPLICATION NUMBER: 60/217, PRIOR FILING DATE: 2000-06-18 PRIOR FILING DATE: 2000-07-11 PRIOR APPLICATION NUMBER: 60/225, PRIOR APPLICATION NUMBER: 60/226, PRIOR APPLICATION NUMBER: 60/227, PRIOR APPLICATION NUMBER: 60/226, PRIOR APPLICATION NUMBER: 60/227, PRIOR APPLICATION NUM	Qy 141 TCGAGACCATCCTGGCCAACATGGTGA 2377 TTGAGACAACCATGCTGGCCAACATGGTGA 201 TGGGCATGGTGGCCAACACATGGTGAT Qy 201 TGGGCATGGTGGCCACACCTGTAGTC
7-11 60/225,447 60/218,290 7-14 60/225,757 8-14 8-12 8-14 8-12 60/226,868 8-22 60/216,647 7-07 60/225,267 8-14 60/225,270 8-14 60/225,270 8-14 60/225,270 8-14 60/225,270 60/225,270 60/225,270 60/235,834 9-21 60/234,274 9-21 60/234,223 9-21 60/234,223 9-21 60/228,924	US/10074095 7704A1 21C Acids, Proteins, and Antibodies R: US/10/074,095 22-02-14 22-02-14 21-07-17 21-07-1860 21-17 21-07-1886 22-04 22-04 22-04 22-04 22-04 22-04 23-04	TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAATACAAAAAATACCCCATCTTTACTAAAATACAAAAAA
PRIOR APPLICATION NUMBER: 60/237,038 PRIOR FILING DATE: 2000-10-02 PRIOR FILING DATE: 2000-10-02 PRIOR FILING DATE: 2000-09-29 PRIOR APPLICATION NUMBER: 60/236,802 PRIOR APPLICATION NUMBER: 60/237,037 PRIOR FILING DATE: 2000-10-02 PRIOR APPLICATION NUMBER: 60/237,040 PRIOR APPLICATION NUMBER: 60/237,040 PRIOR APPLICATION NUMBER: 60/240,960 PRIOR FILING DATE: 2000-10-02 PRIOR FILING DATE: 2000-10-02 PRIOR PILING DATE: 2000-10-13 PRIOR FILING DATE: 2000-10-13 PRIOR PRILING DATE: 2000-10-13 PRIOR APPLICATION NUMBER: 60/241,787 PRIOR FILING DATE: 2000-11-08 PRIOR APPLICATION NUMBER: 60/246,474 PRIOR APPLICATION NUMBER: 60/246,532 PRIOR APPLICATION NUMBER: 60/249,216 PRIOR APPLICATION NUMBER: 60/249,216 PRIOR APPLICATION NUMBER: 60/249,216 PRIOR APPLICATION NUMBER: 60/249,216 PRIOR PILING DATE: 2000-11-17 PRIOR APPLICATION NUMBER: 60/249,216 PRIOR APPLICATION NUMBER: 60/249,216 PRIOR APPLICATION NUMBER: 60/249,216 PRIOR APPLICATION NUMBER: 60/249,216 PRIOR PILING DATE: 2000-11-17 PRIOR PILING DATE: 60/226,681	PRIOR APPLICATION NUMBER: 60/236,368 PRIOR FILING DATE: 2000-09-29 PRIOR FILING DATE: 2000-12-08 PRIOR PPLICATION NUMBER: 60/251,868 PRIOR PPLICATION NUMBER: 60/259,344 PRIOR FILING DATE: 2000-12-08 PRIOR APPLICATION NUMBER: 60/229,344 PRIOR APPLICATION NUMBER: 60/234,997 PRIOR APPLICATION NUMBER: 60/229,343 PRIOR APPLICATION NUMBER: 60/229,343 PRIOR APPLICATION NUMBER: 60/229,345 PRIOR APPLICATION NUMBER: 60/229,345 PRIOR APPLICATION NUMBER: 60/229,345 PRIOR APPLICATION NUMBER: 60/229,287 PRIOR APPLICATION NUMBER: 60/229,287 PRIOR APPLICATION NUMBER: 60/229,287 PRIOR APPLICATION NUMBER: 60/229,513 PRIOR APPLICATION NUMBER: 60/229,513 PRIOR APPLICATION NUMBER: 60/231,413 PRIOR APPLICATION NUMBER: 60/231,413 PRIOR APPLICATION NUMBER: 60/231,413 PRIOR APPLICATION NUMBER: 60/231,413 PRIOR APPLICATION NUMBER: 60/237,039	PRIOR APPLICATION NUMBER: 60/224,518 PRIOR FILING DATE: 2000-08-14 PRIOR APPLICATION NUMBER: 60/236,369 PRIOR PILING DATE: 2000-09-29 PRIOR PILING DATE: 2000-09-14 PRIOR APPLICATION NUMBER: 60/224,519 PRIOR APPLICATION NUMBER: 60/220,964 PRIOR FILING DATE: 2000-07-26 PRIOR PILING DATE: 2000-07-26 PRIOR PILING DATE: 2000-07-26 PRIOR PPLICATION NUMBER: 60/241,809 PRIOR APPLICATION NUMBER: 60/249,299 PRIOR APPLICATION NUMBER: 60/249,299 PRIOR APPLICATION NUMBER: 60/249,299 PRIOR APPLICATION NUMBER: 60/236,327 PRIOR FILING DATE: 2000-11-17 PRIOR PILING DATE: 2000-10-20 PRIOR APPLICATION NUMBER: 60/241,785 PRIOR APPLICATION NUMBER: 60/241,617 PRIOR APPLICATION NUMBER: 60/244,617 PRIOR APPLICATION NUMBER: 60/244,617 PRIOR APPLICATION NUMBER: 60/244,617 PRIOR

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OR FILING DATE: 2000-09-08
OR APPLICATION NUMBER: 60/232,080
OR FILING DATE: 2000-09-08
OR APPLICATION NUMBER: 60/231,414
OR FILING DATE: 2000-09-08
OR FILING DATE: 2000-09-08
OR APPLICATION NUMBER: 60/231,244
OR FILING DATE: 2000-09-08
OR APPLICATION NUMBER: 60/233,064
DR FILING DATE: 2000-09-14

DR APPLICATION NUMBER: 60/241,808

DR FILING DATE: 2000-10-20

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DR APPLICATION NUMBER: 60/241,786

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DR FILING DATE: 2000-11-17

DR APPLICATION NUMBER: 60/249,211

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DR APPLICATION NUMBER: 60/249,215

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DR FILING DATE: 2000-11-17
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APPLICATION NUMBER: 60/231,242
FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/232,081
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/232,400
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APPLICATION NUMBER: 60/232,401
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FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/232,397
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,214
FILING DATE: 2000-11-17
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,244
FILING DATE: 2000-11-17
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FILING DATE: 2000-06-30
APPLICATION NUMBER: 60/225,266
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APPLICATION NUMBER: 60/230,438
FILING DATE: 2000-09-06
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FILING DATE: 2000-08-14
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APPLICATION NUMBER: 60/225,759
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SEQ ID NO 797
LENGTH: 32146
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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Best Local Similarity
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TITLE OF INVENTION: Nucleic Acids, Proteins, EILE REFERENCE: PC008C2
CURRENT APPLICATION NUMBER: US/10/212,872
CURRENT FILING DATE: 2002-08-07
Prior application removed - See File Wrapper NUMBER OF SEQ ID NOS: 1198
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PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08
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CTTGAACCCGGGAGGCGGAGGTTGCAATGAGCCGAGATTGTACTACTGCAATGCAGAGAC
                                                                                    TGGGCATGGTGGCACACACCTGTAGTCCCCAGCTACTCAGGAG-------CCGGAGATTGC
                                                                                                                               TTGAGACAAGCCTGGCCAACATGGTGAAACCCCTGTCTCTACTAAAAAATACAAAAATTAGC
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                                                                 AGGGCÁTGGTGGCGGGCÁCCTGTÁGTCCCAGCTGCTTGGGÁGACTGAGCCAGGÁGÁATTG 2258
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Pred. No. 4.2e-35;
1; Mismatches 95;
                                                                                                                                                                                                                                                                              Score 150.6; DB 7
Pred. No. 4.2e-35;
                                                                                                                                                                                                                                                               Mismatches
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APPLICANT: COMPALION:
APPLICANT: COHEN, Irun R.
APPLICANT: BESERMAN, Pierre
APPLICANT: BESERMAN, Pierre
APPLICANT: MOSONEGO, Alon
APPLICANTON: ACTIVARTED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
FILE REPERENCE: E1S-SCHWARTS-2A
CURRENT FILING DATE: 1201-06-28
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR APPLICATION NUMBER: US 09/218,277
PRIOR APPLICATION NUMBER: 1124500
PRIOR FILING DATE: 1998-07-21
PRIOR FILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
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Search completed: July 17, Job time : 1466 secs
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US-09-893-348-9/c
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37.6%;
Best Local Similarity 72.1%;
Matches 196; Conservative
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ORGANISM: Homo sapiens
-09-893-348-9
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                                                                                                                                                                                                                                            261 TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
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                                                                                                                              CAAAAACAACAACAAAAAAACCATA 352
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                      2006, 22:44:38
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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPERIOE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
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195150,
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23292, A
28242, A
22659, A
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160262,
220429,
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405873,
476919,
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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION UNMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR PRILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR FILING DATE: 2004-11-03

PRIOR PRILING DATE: 2004-11-03
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Best Local S
Matches 218
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RESULT 2
US-11-266-748A-204137/c
; Sequence 204137, Application US/11266748A
; Publication No. US20060134663A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.
SEQ ID NO 23004
LENGTH: 216387
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR APPLICATION NUMBER: EP 04105485.9
OR RILING DATE: 2004-11-03
OR APPLICATION NUMBER: EP 04105484.2
OR APPLICATION NUMBER: EP 0405484.2
OR APPLICATION NUMBER: US 60/662,276
OR APPLICATION NUMBER: US 60/700,293
OR APPLICATION NUMBER: US 60/700,293
OR FILING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                   195718 CTTGAACCTGAGAGGCAGAGGGTGCAGTGAACCAAGATACTCCAGCCTAGTGACACAGCG 195777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 TOGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAAATAGC
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Pred. No. 9.5e-24;
1; Mismatches 53
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PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2005-07-16
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
SEQ ID NO 204137
LENGTH: 1000
                                                                                                                                                                             PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
                                                                              SEQ ID NO 391815
LENGTH: 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 391815, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
TYPE: DNA
ORGANISM: Homo Sapiens
-11-266-748A-391815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 205-11-03
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ORGANISM: Homo Sapiens
-11-266-748A-204137
                                                                                                                                     SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
                                                                                                                                                     PHIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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Local Similarity 74.4%;
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Pred. No. 7.2e-23;
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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION UMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PRILING DATE: 2004-11-03
PRIOR PRILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: BP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: BP 04105484.2
PRIOR PRILING DATE: 2004-11-03
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PRIOR APPLICATION NUMBER: BP 04105484.2
PRIOR PRILING DATE: 2004-11-03
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; Sequence 482533, Application US/11266748A
; Publication No. US20060134663A1
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Best Local
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
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                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1000
                                                                                                                                                                                                                       local Similarity
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                            TCGAGACCATCCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAAATACAAAAAAATAGC
                                                                                            ACGCCTGTAATCCCAGCACTTTGGGAGGTCAACGTGGGCAGATCACTTGAGTTCAGGAGT 210
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Mulligan, Karl
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Pred. No. 1.6
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Pred. No. 1.6e-22;
1; Mismatches 62;
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1es 62;
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US-11-266-748A-118317
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ORGANISM: Homo Sapiens
-11-266-748A-118317
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
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APPLICANT: Johnston, Patr:
APPLICANT: Mulligan, Karl
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SOFTWARE: PatentIn version 3
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APPLICATION NUMBER: EP 04105507.0
FILING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105485.9
FILING DATE: 2004-11-03
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FILING DATE: 2004-11-03
APPLICATION NUMBER: US 60/662,276
FILING DATE: 2005-03-14
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ATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAAA
                                                              CAGGCACCTGTAATCCCAGGTACTAGGGAGGCTTTTGAACCCAGGAGGCAGAGGTTGCAG
                                                                                               CACACACCTGTAGTCCCAGCTACTCAGGAG-----CCGGAGATTGCAGTGAGCTGAG
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Pred. No. 3.4e
1; Mismatches
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 0410568.6
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US-11-266-748A-160481/c
; Sequence 160481, Application US/11266748A
; Publication No. US20060134663A1
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; ORGANISM: Homo Sapiens
US-11-266-748A-160481
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
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hes 221;
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Pred. No. 3.4e-22;
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RESULT 8
US-11-266-748A-474173/c

US-11-266-748A-474173, Application US/11266748A

| Publication No. US20060134663A1
| GENERAL INFORMATION:
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PRIOR FILING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105485.9
PRIOR PELICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PELICATION NUMBER: US 00/662,276
PRIOR PELICATION NUMBER: US 06/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
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LENGTH: 1000
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    APPLICANT: Harkin, Paul APPLICANT: Johnston, F
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NUMBER OF SEQ ID NOS: 483996
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
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Johnston, Patrick
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Pred. No. 3.4e-22;
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US-11-319-952-56
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Matches 221;
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LENGTH: 1000
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TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
CURRENT FILING DATE: PD 04105479.2
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
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PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
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ORGANISM: Homo Sapiens
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Pred. No. 3.4e-22;
1; Mismatches 93
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Sequence 56, Application US/11319952
Publication No. US20060134114A1
GENERAL INFORMATION:
APPLICANT: Yousef, George M.
APPLICANT: Diamandis, Eleftherios
TITLE OF INVENTION: Novel Human Kallikrein-Like

FILE REFERENCE: MTS3USA
CURRENT APPLICATION NUMBER: US/11/319,952
CURRENT FILING DATE: 2005-12-28
PRIOR APPLICATION NUMBER: US/09/936,271
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: PCT/CA00/00258

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RESULT 10
US-11-266-748A-219455
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-319-952-56
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Best Local Similarity
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Publication No. US20060134663A1
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                   SOFTWARE: PatentIn version SEQ ID NO 219455
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (31918)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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                                                                                                                     PRIOR APPLICATION NUMBER: EP 04105484.2 PRIOR FILING DATE: 2004-11-03 PRIOR REPLICATION NUMBER: US 60/662,276 PRIOR FILING DATE: 2005-03-14
                                                              NUMBER OF SEQ ID NOS: 483996
                                                                               PRIOR FILING DATE: 2005-07-18
                                                                                                    PRIOR APPLICATION NUMBER: US 60/700,293
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: EP 04105479.2
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75.4%;
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Pred. No. 4.2e-22;
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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PRIOR DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
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US-11-266-748A-239441/c
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Best Local
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                                              Matches
                                                                               Query Match
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APPLICANT: Johnst
APPLICANT: Mullig
                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: EP 04105484.2 PRIOR FILING DATE: 2004-11-03 PRIOR APPLICATION NUMBER: US 60/662,276 PRIOR FILING DATE: 2005-03-14
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 483996
                                                                                                                                     TYPE: DNA ORGANISM: Homo Sapiens
                                                                                                                                                                            LENGTH:
                                                              Local Similarity
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ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
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Mulligan, Karl
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75.4%;
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                                              Score 147.2; | Pred. No. 4.4e
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Pred. No. 4.4e-22;
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                                                                4.4e-22;
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ACGCCTGTAATCCTAGCACTTTGGGAGGCCGAGGCAGGTGGATCACCTGAGGTCAGGAGT 246

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Sequence 1113, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT TILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
ROCEMENT FILING DATE: 2002-03-28
                                                                                                                 RESULT 13
US-11-266-748A-23290/c
US-11-266-748A-23290/c
| Sequence 23290, Application US/11266748A
| Publication No. US20060134663A1
| GENERAL INFORMATION:
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US-11-293-697-1113/c
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SEQ ID NO 1113
LENGTH: 2909
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                                                APPLICANT: Harkin, Paul
APPLICANT: Johnston, P
APPLICANT: Mulligan
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ORGANISM: Homo sapiens
-11-293-697-1113
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
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nes 192; Conservative
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Pred. No. 5.2e-22;
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US-11-266-748A-23290
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PRIOR FILLING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105507.0
PRIOR PELICATION NUMBER: EP 04105507.0
PRIOR PELICATION NUMBER: EP 04105485.9
PRIOR PELICATION NUMBER: EP 04105484.2
PRIOR PELICATION NUMBER: EP 04105484.2
PRIOR PELICATION NUMBER: EP 04105484.2
PRIOR PELICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PELING DATE: 2005-07-18
PRIOR FILLING DATE: 2005-07-18
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SEQ ID NO 23290
                                                                                                                                                                                                                                                                                                                                                                                 Matches 175;
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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                                                                                                                                                                                                                                                                                                                                                                                                  Match 36.6%;
Local Similarity 78.5%;
23309
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TTTGAACGCGGGTTGCGAAGGTTGCAGTGAGCCGAGATTGCGC
                                              TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGC 303
                                                                                             CGGGCATGGTGGTGCACGCCTGTAGTCCCAGCTACTCGGGAGGCGGAGGCAGGAGAATCA
                                                                                                                                            TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCCGAGATTGCAGTGAGC
                                                                                                                                                                                                                                    TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
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Pred. No. 9.1e-22;
0; Mismatches 48;
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Gaps

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260

23310

200

23430

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Johnston, Patrick

APPLICANT: Mulligan, Karl

ITILE OF INVENTION: Transcriptome Microarray Technology and

ITILE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR APPLICATION NUMBER: EP 04105483.9

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR APPLICATION NUMBER: EP 04105484.2 RESULT 14 US-11-266-748A-30503/c ; Sequence 30503, Application US/11266748A ; Publication No. US20060134663A1 FILING DATE:

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USF11-266-748A-24156/c
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; TYPE: DNA; Homo Sapiens; ORGANISM: Homo Sapiens US-11-266-748A-24156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24156, Application US/11266748A Publication No. US20060134663A1
                                                                 SEQ ID NO 24156
LENGTH: 3324
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PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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                                                                                                                                PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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PRIOR ETLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
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                                                                                                                SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: EP 04105483.4 PRIOR FILING DATE: 2004-11-03
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ORGANISM: Homo Sapiens
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                                                                                                                                                                                                    FILING DATE: 2004-11-03
APPLICATION NUMBER: US 60/662,276
FILING DATE: 2005-03-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKC
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72.7%;
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Pred. No. 1.1e-21;
wismatches 70;
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RESULT 16
US-11-266-748A-390100
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PRIOR FILLING DATE: 2004-11-03
PRIOR PELLING DATE: 2004-11-03
PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2005-03-14
PRIOR FILLING DATE: 2005-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 390100, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                                               SEQ ID NO 390100
                                                                                                                                                         Matches
                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                          Query Match
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
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                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 483996
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                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                         434 ACACAATTTTACATTAAGAAATACTGTGCAGGCCATGCGTGGTGGCTCAGGCCTGTAATC
                                    93
                                                                                                              33 ACCCAAATATTAATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCTGTAATC
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CCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACCGGAGGTCAGGAGTTCGAGACCAGCC
                                  CCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCATCC
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Mulligan, Karl
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Pred. No. 1.4e
l; Mismatches
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Pred. No. 1.4e-21;
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                                                                                                                                                                                            DB 8;
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153 494

TGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGGATGGTGG

212 553

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RESULT 17
US-11-266-748A-480818/c
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PRIOR FILING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR PRILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
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Best Local Similarity
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APPLICANT: Mulligan, Karl'
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
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SOFTWARE: PatentIn version 3.3
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TYPE: DNA
ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                      CCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACCGGAGGTCAGGAGTTCGAGACCAGCC
                                                                                                                                                                                                                                                                                     CCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCATCC 152
                                                                                                                                                                                                                                                                                                                                  ACACAATTTTACATTAAGAAATACTGTGCAGGCCATGCGTGGTGGCTCAGGCCTGTAATC
                                                                           CACACACCTGTAGTCCCAGCTACTCAGGAG------CCGGAGATTGCAGTGAGCTGAG
                                                                                                                                         TTGCCAACATAGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCCGGGCATGGTGG
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ATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAAA 324
                                             CAGGCACCTGTAATCCCAGCTACTAGGGAGGCTTTTGAACCCAGGAGGCAGAGGTTGCAG
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Pred. No. 1.4e-21;
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US-11-266-748A-206136/c
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; ORGANISM: Homo Sapiens
US-11-266-748A-60135
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US-11-266-748A-60135
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PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
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GENERAL INFORMATION: APPLICANT: Harkin,
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Matches 178;
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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Pred. No. 2.2e-21;
D; Mismatches 56
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US-11-266-748A-60135/c
Sequence 60135, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
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PRIOR PILLING DATE: 2004-11-03
PRIOR PELLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILLING DATE: 2004-11-03
PRIOR PILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILLING DATE: 2005-03-14
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Matches
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            APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
ITTLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-012 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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APPLICANT: Johnston, P
APPLICANT: Mulligan, K
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ORGANISM: Homo Sapiens
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APPLICATION NUMBER: EP 04105483.4
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Pred. No. 1.9e-21;
0; Mismatches 83
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; Sequence 198112, Application US/11266748A
; Publication No. US20060134663A1
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Best Local :
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105507.0
                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319198) CURRENT APPLICATION NUMBER: US/11/266,748A CURRENT FILING DATE: 2005-11-03
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Harkin, Paul
APPLICANT: Johnston, P
APPLICANT: Mulligan, K
                                                                        PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
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ORGANISM: Homo Sapiens
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les 217; Conserv
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                 FILING DATE: 2004-11-03
APPLICATION NUMBER: US 60/662,276
FILING DATE: 2005-03-14
APPLICATION NUMBER: US
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Mulligan, Karl
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73.6%;
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Pred. No. 2.5e-
1; Mismatches
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RESULT 22
US-11-266-748A-59101/c
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
                                                                               Query Match
Best Local Similarity
Matches 155; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 59101, Application US/11266748A Publication No. US20060134663A1
                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo Sapiens
-11-266-748A-59101
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Best Local Similarity
Matches 173; Conserv
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SOFTWARE: PATEMETH VETSION 3.3
SEQ ID NO 198112
LENGTH: 1000
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ORGANISM: Homo Sapiens
-11-266-748A-198112
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102/ (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 483996
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LENGTH: 96217
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                                                                                   Score 143; DB 8;
Pred. No. 4.2e-21;
0; Mismatches 20
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
CURRENT APPLICATION NUMBER: EP 04105479.2
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PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
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APPLICANT: Johnston, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 1945
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FILING DATE: 2005-03-14
APPLICATION NUMBER: US 60/700,293
FILING DATE: 2005-07-18
R OF SEQ ID NOS: 483996
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ilarity 69.4%;
Conservative
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Pred. No. 4.2e-21;
1; Mismatches 85
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US-11-266-748A-28208
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PRIOR FILING DATE: 2004-11-03
PRIOR PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PRIOR PATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 0410507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PRIOR DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
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TYPE: DNA
ORGANISM: Homo Sapiens
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Pred. No. 4.2
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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
FITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
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SOFTWARE: Patentin version 3.3
SEQ ID NO 28208
LENGTH: 1477-1
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LOCATION: (836909)..(836909)
OTHER INFORMATION: n is a, c
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NAME/KEY: misc_feature
LOCATION: (414394)..(414394)
OTHER_INFORMATION: n is a, c
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LOCATION: (1041105)...(1041105)
OTHER INFORMATION: n is a, c,
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1070083 AATCTGGGAGGCGGAGGTTGCAGTCTTTAGCATGGGTGACAGAGTGAGATTCTGTCTTAG 1070142
                                                                                          1070023
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                                          264 GATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAA 323
                                                                                                                                   205 CATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGA-GCCGGAGATTGCAGTGAGCTGA 263
                                                                                                                                                                                                                                                                                                                      85 CTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGA 144
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                                                                                          TTTGGTGGTGTGTGCCTGTAGTCCCAGCTACCCAGGAGGCTGAAGCAAGAGAATCGCTTG 1070082
                                                                                                                                                                                   GACCAGCCTGGCCCACATGGTGAAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGG
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Pred. No. 5.8e-21;
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324

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350

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RESULT 27

US-11-266-748A-292231/c

US-11-266-748A-292231, Application US/11266748A

Publication No. US20060134663A1

| GENERAL INFORMATION:
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U$-11-266-748A-223929/c
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PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
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Best Local S
Matches 207
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ORGANISM: Homo Sapiens
-11-266-748A-223929
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SOFTWARE: PatentIn version 3
SEQ ID NO 223929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Transcriptome Microarray Technology TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Harkin, Paul
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                                                                                                                                                                                                                                                       AACCCAGGAGGCGAGATCATGCCATTGCACTCCAGCCTGGGTGACAGAGTGAAACTCTGT
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Mulligan, Karl
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Pred. No. 4.5e-21;
1; Mismatches 82;
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PRIOR FILLING DATE: 2004-11-03
PRIOR PELLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR TILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILLING DATE: 2004-11-03
PRIOR PELLING DATE: 2005-03-14
PRIOR PELLING DATE: 2005-03-14
PRIOR PELLING DATE: 2005-07-18
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Best Local S
Matches 207
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT PRILICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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ORGANISM: Homo Sapiens
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                               .CTCAAAAACAACAACAAAAAAACAAAAAAACCATAAGACATTGTCCATCTGCGGTTC
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CTCAAAAAAAAAAAAAAAAAGAAAAGTTCCCTTACTGTGCCTACTTGCCCCTC
                                                                                               AACCCAGGAGGCGAGATCATGCCATTGCACTCCAGCCTGGGTGACAGAGTGAAACTCTGT
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Pred. No. 4.5e-21;
1; Mismatches 82
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RESULT 28
US-11-266-748A-293957
Sequence 293957, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILL REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03

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RESULT 29
US-11-266-748A-343660
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PRIOR FILLING DATE: 2004-11-03
PRIOR PELLOATION NUMBER: US 60/662,276
PRIOR FILLING DATE: 2005-03-14
PRIOR FILLING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILLING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 343660, Application US/11266748A publication No. US20060134663A1 GENERAL INFORMATION:
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ORGANISM: Homo Sapiens
-11-266-748A-293957
                                                                                                                                                                                                                                                                 APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
                                                                                                            PRIOR PRIOR
                                                                                                                                                    PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
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ENGTH: 1000
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                                          APPLICATION NUMBER: EP 04105485.9 FILING DATE: 2004-11-03 APPLICATION NUMBER: EP 04105484.2 FILING DATE: 2004-11-03
                                                                                                                                 FILING DATE: 2004-11-03
APPLICATION NUMBER: US 60/662,276 FILING DATE: 2005-03-14
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Pred. No. 4.5e-
1; Mismatches
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Methods of Using the Same
FILE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
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US-11-266-748A-345386/c
US-11-266-748A-345386, Application US/11266748A
; Publication No. US20060134663A1
; Publication No. US20060134663A1
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                                                               ; ORGANISM: Homo Sapiens
US-11-266-748A-345386
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NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 343660
LENGTH: 1000
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                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/700,293 PRIOR FILING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: EP 04105485.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                595 GACCAGCCTGGCCAACACGGTGAAACCCCCATCTCTGCTAAAAATACAAAAATTAGCTGGG
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73.0%;
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Query Match Best Local Similarity

Pred. No. 4.5e-21;

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RESULT 31

W3-11-266-748A-403868/c

; Sequence 403868, Application US/11266748A

; Publication No. US20060134663A1
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: UP 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR PILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-03-18
PRIOR PILING DATE: 2005-03-18
PRIOR PILING DATE: 2005-03-18
                                                                                                                                                                                                                   Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                     -11-266-748A-403868
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Johnston, Patrick APPLICANT: Mulligan, Karl
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
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                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo Sapiens
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205 CATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAG
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                                          GACCAGCCTGGCCAACACGGTGAAAACCCCCATCTCTGCTAAAAATACAAAATTAGCTGGG
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Pred. No. 4.5e
1; Mismatches
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.7
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US-11-266-748A-406117
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PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILLING DATE: 2005-03-14
PRIOR FILLING DATE: 2005-07-18
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Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version
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TYPE: DNA
373
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GTGAGCAGAGTGAGACKCCGTCTCAAAAAACAACAACAAAAAAACAAAAAAAACCATAAGACA 357
                                                                                       CTTGAACTGGGGAGGCAGAGGTTGCAGTGAGACAAGATCACGTCACTGTACTCCAGCCTG 372
                                                                                                                                 AGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCA-----CAGA
                                                                                                                                                                                                                                TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGA-----GCCGGAGATTGC 253
                                                                                                                                                                                                                                                                                                                                                                                                                  ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                  TGGGCATGATGGCAGGCACCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTG 312
                                                                                                                                                                                                                                                                               TCGAGACCAGCCTGGCCAACATGGTGAAACCCCCGTCTCTATTAAAAATACAAAATTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 142.4; DB 8;
Pred. No. 4.5e-21;
1; Mismatches 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1000;
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RESULT 34
US-11-266-748A-477163/c
US-11-266-748A-477163, Application US/11266748A
publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
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US-11-266-748A-474914
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; ORGANISM: Homo Sapiens
US-11-266-748A-474914
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PRIOR FILLING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105483.4
PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILLING DATE: 2004-11-03
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Best Local Similarity
Matches 207; Conserv
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Publication No. US20060134663A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189) CURRENT APPLICATION NUMBER: US/11/266,748A CURRENT FILING DATE: 2005-11-03 PRIOR APPLICATION NUMBER: EP 04105479.2 PRIOR FILING DATE: 2004-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: EP 04105484.2 PRIOR FILING DATE: 2004-11-03 PRIOR APPLICATION NUMBER: US 60/662,276 PRIOR FILING DATE: 2005-03-14
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SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/700,293 PRIOR FILING DATE: 2005-07-18
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
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                                                                                                                                                                                                                                                                                             CTCAAAAACAACAAAAAAAAAAAAAAACCATAAGACATTGTCCATCTGCGGTTC 374
                                                                                                                                                                                                                                                                                                                                      AACCCAGGAGGCGAGATCATGCCATTGCACTCCAGCCTGGGTGACAGAGTGAAACTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                        CGTGGTGGCAGGCGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACCAGCCTGGCCAACACGGTGAAACCCCCATCTCTGCTAAAAATACAAAAATTAGCTGGG
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Mulligan, Karl
                                                                                                                                                                                                                                                       CTCAAAAAAAAAAAAAAAGAAAAGTTCCCTTACTGTGCCTACTTGCCCCTC
                                                                                                                                                                                                                                                                                                                                                                               ATCGCAGAGTGAGCCGAAATCACAGATCA-----CAGAGTGAGCAGAGTGAGACKCCGT 318
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; Pred. No. 4.5e
1; Mismatches
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105482.6
PRIOR PELICATION NUMBER: EP 04105483.4
PRIOR PELICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 06700,293
PRIOR PILING DATE: 2005-03-14
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US-11-191-644-1
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US-11-266-748A-477163
                                                      APPLICANT: MICHAUD, GREG
APPLICANT: MICHAUD, GREG
TITLE OF INVENTION: COMPOSITIONS, KITS AND I
TITLE OF INVENTION: COMPOSITIONS, KITS AND I
TITLE OF INVENTION: UNRECTED TO CORTACTIN I
FILE REFERENCE: INV-1007-UT
CURRENT APPLICATION NUMBER: US/11/191,644
CURRENT FILING DATE: 2005-07-27
PRIOR APPLICATION NUMBER: 60/591,827
PRIOR FILING DATE: 2004-07-27
NUMBER OF SEQ ID NOS: 29
CONTENTION DATE: 2004-07-27
                                                                                                                                                                                                                                                                                                Sequence 1, Application US/11191644
Publication No. US20060141529A1
GENERAL INFORMATION:
APPLICANT: KOLESKE, ANTHONY JOHN
APPLICANT: BOYLE, SCOTT NILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version SEQ ID NO 477163
                  SOFTWARE: PatentIn version 3.3 SEQ ID NO 1
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Best Local Similarity
                                                                                                                                                                                                                                                           APPLICANT:
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TYPE: DNA
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LENGTH: 157866
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                                                                                                                                                                                                                                                                                BOYLE, SCOT
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TZEŖ, BARRY
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Pred. No. 4.5e-21;
l; Mismatches 57
                                                                                                                                                                                             CORTACTIN
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AND AN
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Publication No. US20066105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION UNMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
TENETH: 2800
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Best Local Similarity
Matches 229; Conserv
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens -11-293-697-23
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ORGANISM: Homo
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                                                                                                                                                                                      136 AGAGATCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAA 195
                                                                                                                                                                                                                                         847 GTTTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCAGGTGGATCACCTGAGGTCA
                                                                                                                                                             787 GGAGTTCGAGACCAGCCTGGCCAACATGGTGAAAACCCCGTCTCTACTAAAAAATACAAAAA
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                                     256 TGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKC 315
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AATCACTGGAACCCGGGAGGCGGAGGCCTC----CAGTCTAGTCAAAAAAAAGCAAGACTC
                                                                                                                                                                                                                                                                      GCTGAATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGGGGGATCACCTGAGGTCA 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCAGGCGGATCAC--GAGGTCAAGAGA
                                                                               TTAGCTGGGCGTGGTGCACATGCCTGTAATCCCCAGCTACCCGGGAGGCTGAGGCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCATCTGCGG 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTGCATGGTGGTGCACGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTCTACTAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
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73.6%;
                                                                                                                                                                                                                                                                                                                                         Score 142; DB 8;
Pred. No. 5.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 142.2; DB 7
Pred. No. 6.3e-21;
                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59;
                                                                                                                                                                                                                                                                                                                                                              Length 2800;
                                                                                                                                                                                                                                                                                                                           Indels
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; ORGANISM: Homo
US-11-293-697-604
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US-11-293-697-604/c
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SEQ ID NO 604
LENGTH: 3252
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Publication No. US20
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVel full length cDN:
FILE REFERENCE: HI-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
                                                                                                                                                                                                                                                                                              Local Similarity
les 172; Conserv
2758 TGAGATCATGCCACTGCCCTCCAGCGTGGGCGACAGAGTGAG 2717
                                                                        2818 CAGGCGTGGTGCTGCCTGTAATCCCAGCTACTCGAGAGGCTGAGGTTGCAGTGAGC
                                                                                                                                                 2878
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                                  TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAG 302
                                                                                                 TGGGCATGGTGGCACACACCTGTAGTCCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGC
                                                                                                                                               TTGAGACCAGCCTGGCCAACATGGTGAAACCCCCGTCTCTACTAATAAAACAAAAATTAGC
                                                                                                                                                                        TCGAGACCATCCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAATAACAAAAAAATAGC
                                                                                                                                                                                                                    ACGCCTGTAATCCCAGTACTTTGGGAGGCTGAGGGAGGTGGATCACGTGAGGTCAGGAGT
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                                                                                                                                                                                                                                                          ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
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o. US20060105376A1
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                                                                                                                                                                                                                                                                                                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                              35.5%;
                                                                                                                                                                                                                                                                                            Score 142; DB 8;
Pred. No. 5.7e-21;
D; Mismatches 50
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                                                                                                                                                                                                                                                                                                                               Length 3252;
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                                                                                                                                                                                                                                                            140
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RESULT 38

US-11-266-748A-202571
US-11-266-748A-202571
Sequence 202571, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:
APPLICANT: HARKIN, Paul

APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 0405484.2
PRIOR APPLICATION NUMBER: US 04105484.2
PRIOR APPLICATION NUMBER: US 04662,276

PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996

SOFTWARE: PatentIn version 3.3

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US-11-266-748A-23004/c
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LENGTH: 1000
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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                                           -11-266-748A-23004
                                                                                                                                                                PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo Sapiens
-11-266-748A-202571
                                                                                                                                                 SOFTWARE: Patentin
                                                                                                                                                                                                                                                       PRIOR
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
                                                               TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                      LENGTH: 216387
                                                                                                                              ID NO 23004
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                                                                                                                                                                                                                                                   APPLICATION NUMBER: EP 04105485.9
FILLING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105484.2
FILLING DATE: 2004-11-03
APPLICATION NUMBER: US 60/662,276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCTCAAAAACAACAACAAAA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAACTTGGGAGGTGAAGGTTGCAGTAAGCCACTCCAGCCTGGGTGACAGAGTGAGACTTT 622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCTGGAATTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCATGGTGGCACATGTTTGTAATCCCAGCTACTTTGGGAGGCTGAGGCAGGAGAATCACTT 562
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  35.4%;
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Pred. No. 6.5e-21;
1; Mismatches 60
    Score 141.6;
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    DB
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Length 216387;
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR TILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 201568, Application US/11266748A Publication No. US20060134663A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 69. Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                             SEQ ID NO 201568
                                                                                                                                                               Matches
                                                                                                                                                                                  Query Match
Best Local
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 48399
SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US
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PRIOR APPLICATION NUMBER: EP 04105484.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: EP 04105507.0 PRIOR FILING DATE: 2004-11-03 PRIOR APPLICATION NUMBER: EP 04105485.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Transcriptome Microarray Technology TITLE OF INVENTION: Methods of Using the Same
                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                             Local Similarity
es 172; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87783
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/662,276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2004-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126
  371
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                                       86
                                                                                                                                                                                                                                                                                                          632
                           TGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAG 145
                                                                                                       CATGGGAACCCAAATATTAATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATATAAAAATTAGTCGGGCATGGTGGCACATGCCTGTAATCCCAGCTACTCATGAGGCT 87724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAACCCCCGTCTCTACTAAA
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                                                                               CAGGGGAGGGAAGTTATGTGCCAAAAAGTACCAGGCCAĞĞCAGGCGCGATGGCTCACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTGAGACKCCGTCTCAAAAACAACAACAAAAAAAAAAA 343
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                                                                                                                                                               Conservative
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1; Mismatches 85;
                                                                                                                                                             Score 141.4; DB Pred. No. 7e-21; O; Mismatches
                                                                                                                                                                                                     DB 8;
                                                                                                                                                               51;
                                                                                                                                                                  Indels
                                                                                                                                                                                                   Length 632;
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ACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGC 205

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RESULT 42
US-10-517-441-32/c
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Matches
                                                                                                       GENERAL INFORMATION:
                                                                                                                         Sequence 32, Application US/10517441
Publication No. US20060121467A1
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ORGANISM: Homo Sapiens
-11-266-748A-59943
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APPLICANT: FOEKENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MAIER, Sabine
APPLICANT: MARTENS, John
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SOFTWARE: PatentIn version 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (31189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
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PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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APPLICATION NUMBER: EP 04105484.2
FILING DATE: 2004-11-03
APPLICATION NUMBER: US 60/662,276
FILING DATE: 2005-03-14
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Mulligan, Karl
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Pred. No. 7.5e-21;
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APPLICANT: Johnston, Patrick

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105499.2

PRIOR APPLICATION NUMBER: EP 04105493.4

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03

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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-517-441-32
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US-11-266-748A-60244
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CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR APPLICATION NUMBER: DE 10345779.4
PRIOR PILING DATE: 2003-01-07
PRIOR PILING DATE: 2002-10-01
                    PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR PRILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR PPLICATION NUMBER: US 60/662,276
PRIOR PILING DATE: 2005-03-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 60244, Application US/11266748A Publication No. US20060134663A1
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SEQ ID NO 32
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APPLICANT: Johnston, P
APPLICANT: Mulligan, K
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Method and nucleic acids
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
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mes 154; Conserv
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SCHMITT, Manfred
LOOK, Maxime P.
MARX, Almuth
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RUJAN, Tamas
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us 60/700,293
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Pred. No. 7.9e-21;
0; Mismatches 21;
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RESULT 44
US-11-266-748A-23291/c
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Query Match
Best Local Similarity
                                                              -11-266-748A-23291
                                                                                                                                              EQ ID NO 23291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo Sapiens
-11-266-748A-60244
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NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                  SOFTWARE: PatentIn
                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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                                                                             LENGTH: 113853
TYPE: DNA
ORGANISM: Homo Sapiens
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OR FILING DATE: 2004-11-03
OR APPLICATION NUMBER: EP 04105483.4
OR FILING DATE: 2004-11-03
OR RILING DATE: 2004-11-03
OR RILING DATE: 2004-11-03
OR FILING DATE: 2004-11-03
OR FILING DATE: 2004-11-03
OR FILING DATE: 2004-11-03
OR APPLICATION NUMBER: EP 04105484.2
OR APPLICATION NUMBER: US 60/662,276
OR FILING DATE: 2004-11-03
OR APPLICATION NUMBER: US 60/662,276
OR FILING DATE: 2005-03-14
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hes 206;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCATGGTGGCACACACCTGTAGTCCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGACCAGCCTGGCCAACATGGCTAAACCCCCGTCTCTACTAAAAATACAAAAATTAGCTGG 23081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAAATACAAAAAATAGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAACCTGGGAGGTTGCAGTGAGCCAAGATCGCACCACTGCACTCCAGCTTGGGC 23201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCATGATGGCACACCTGTATTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCACTT 23141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                      version
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35.4%;
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Pred. No. 9e-21;
1; Mismatches 57;
Score 141.4; DB 8; Pred. No. 9.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 86654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                     Length 113853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
ITITLE OF INVENTION: Transcriptome Microarray Technology and
ITITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-58517
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 172; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.3 SEQ ID NO 58517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 58517, Application US/11266748A Publication No. US20060134663A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Harkin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/700,293 PRIOR FILING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/662,276 PRIOR FILING DATE: 2005-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                              139360 ACGCCTATAATCCCGGCACTTTGGGAGGCCCAGGCAGGTGGATCACCTGAGGTCAGGAGT 139301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108487
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139180 CTTGAACATGGAAGGTGCAGGTTGCAGTGAGCTGAGATTGTGC 139138
                                                                                                                                                                                               139300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: EP 04105484.2 FILING DATE: 2004-11-03
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                                                                                                                                                                                                                                                                                                                       ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGGCATGGTGGCACATGCCTGTAGTCCCAGATACTCGGGAGGCTGAGACAGGAG 108373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGAGACCAGCCTGACCAACAAGGTGAAACCCCCGTCTCTACTAAAAAATACAAAAGTTAGC 108428
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                                                                                                                             TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                         TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAAATAGC 200
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                                              TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGC 303
                                                                                                                                                                                             TCGAGACCAGCCTGGCCAACATGGTGAAACCCCCGTCTCTACTAAAAAACACAAAAATAAGC
                                                                                            TGGGCGTGGTGGCGCACACCTGTAATCCCÁĞCTÁCTCÁĞGÁĞGCTĞÁĞGCAĞGÁĞAATCA 139181
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                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                       Score 141.4; DB b;
Pred. No. 9.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 154394;
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Sequence 24937, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2006-11-03
PRIOR APPLICATION NUMBER: ED 04105479.2
PRIOR FILING DATE: 2004-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HARKIN, Paul
APPLICANT: Mulligan, Karick
APPLICANT: Mulligan, Karick
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 06/662,276
PRIOR PRILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER: DETAILS DATE: 2005-07-18
NUMBER: DETAILS DATE: 2005-07-18
NUMBER: DETAILS DATE: 2005-07-18
NUMBER: DETAILS DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo Sapiens
-11-266-748A-22662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :11-266-748A-22662/c
Sequence 22662, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                   -11-266-748A-24937/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 164429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAAATAGC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCAAGATCGTGC 27390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGC 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGAGACCAGCCTGGCCAACATGGTGAAACCCCCGTCTCTACTAAAAATACAAAAATTAGC
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77.1%;
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Pred. No. 9.3e-21;
0; Mismatches 51;
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; ORGANISM: Homo Sapiens
US-11-266-748A-24937 .
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PRIOR FILLING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105484.2
PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILLING DATE: 2005-03-14
PRIOR PELICATION NUMBER: US 60/700,293
PRIOR FILLING DATE: 2005-07-18
PRIOR FILLING DATE: 2005-07-18
PRIOR FILLING DATE: 2005-07-18
PRIOR FILLING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.3 SEQ ID NO 24937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                     67263
67143 ACAATCACTTGAACCCAGGAGGCGGAGGTTGCAGTGAGCTGAGATTGTGC
                                                                                                                                                                                                                                                                                   67323 GGTGATCATGCCTGTAATCCCAGCACTTTAGGAGGCTGAGGCGGGTGGATCACCTGAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP 04105483.4
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                                                                                                                        194 AAATAGCTGGGCATGGTGGCACACACCTTGTAGTCCCAGCTTACTCAGGAGCCGGAGATTGC 253
                                                                                                                                                                                                                134 CAAGAGATCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197;
                                            254
                                                                                                                                                                                                                                                                                                                               74 TGGCTGAATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGT 133
                                                                                                                                                                                                                                                                                                                                                                                                                          14 CATGTGCTGGGCCATGGGAACCCAAATATTAATAAGACATTGTCAGGCCAGGCATGACAC
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                                         AGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGC 303
                                                                                             AATTAGCCGGGCATGGTGATGTAAGTCTGTAGTCCCAGCTACTCAGGAGGCTGAGGTAGG
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nilarity 67.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 141.2; DB 8
Pred. No. 9.9e-21;
0; Mismatches 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93;
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67094
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GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Johnston, Patrick

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 55815-0102 (139189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR APPLICATION NUMBER: EP 04105483.9

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03 RESULT 48 US-11-266-748A-119261 Sequence 119261, Application US/11266748A Publication No. US20060134663A1 APPLICATION NUMBER: EP 04105484.2 FILING DATE: 2004-11-03 60/662,276

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RESULT 49
US-11-266-748A-161425/c
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                                                          PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR PRIOR DATE: 2004-11-03
PRIOR PELLOATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR PELLOATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
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SEQ ID NO 119261
LENGTH: 1000
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NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 161425
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189) CURRENT APPLICATION NUMBER: US/11/266,748A CURRENT FILING DATE: 2005-11-03
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ORGANISM: Homo Sapiens
·11-266-748A-119261
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PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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Mulligan, Karl
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APPLICANT: Johnston, Patrick

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR APPLICATION NUMBER: EP 04105483.4
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; ORGANISM: Homo Sapiens
US-11-266-748A-161425
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US-11-266-748A-407602
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Best Local
  Query Match
Best Local Similarity
Matches 229; Conserv
                                                                                                                                                                 SOFTWARE: Patent
SEQ ID NO 407602
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APPLICANT: Johnston, F
APPLICANT: Mulligan, K
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PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
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                                                                                                       ORGANISM: Homo Sapiens
                                                                                                                          TYPE: DNA
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milarity 68.8%;
Conservative
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  Score 141; DB 8; Length 1000; Pred. No. 8.7e-21; 1; Mismatches 86; Indels 1
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Pred. No. 8.7e-21;
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Search completed: July 17, 2006, 21:48:24 Job time : 416 secs	364 ATCTGCGGTTCCCAGACTATTGCAGGAGACCAA 396	304 AGAGTGAGACKCCGTCTCAAAAACA 	260 CTGAGATCGCAGAGTGAGCCGAAATCACAGATCACA	201 TGGGCATGGTGGCACACACCTGTAG 	141 TCGAGACCATCCTGGCCAACATGGT	81 ATGCCTGTAATCCCAGCACTTCGGG 200 ACGCCTGTAATCCCAGCACTTTGGG
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